

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 29.7313 Seconds
(without alignments)
268.471 Million cell updates/sec

Title: US-09-928-048A-4

Perfect score: 422

Sequence: 1 VSEIQLMNHLGRHLSMERV.....KSLGRANKADVNVLYKAKSQ 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	98.8	115	1 PTHU	parathyroid hormon
2	366	86.7	115	2 JC4202	parathyroid hormon
3	359	85.1	115	1 PTHO	parathyroid hormon
4	355	84.1	115	1 PTPG	parathyroid hormon
5	311	73.7	115	2 A05091	parathyroid hormon
6	303	71.8	105	2 I51851	parathyroid hormon
7	174.5	41.4	119	2 A34937	parathyroid hormon
8	73	17.3	565	2 G89813	parathyroid hormon
9	72.5	17.2	824	2 F72408	DNA polymerase III
10	72	17.1	1257	1 I58383	leucine-tRNA ligas
11	69.5	16.5	555	2 T44010	retinoblastoma bin
12	67.5	16.0	1156	2 B70356	virion protein [im
13	67	15.9	443	2 E82046	chromosome assembl
14	67	15.9	655	2 C71438	proteinase HslVU,
15	67	15.9	674	2 B71438	hypothetical prote
16	66.5	15.8	378	2 F56653	virion protein - h
17	66	15.6	215	2 T23195	hypothetical prote
18	66	15.6	396	2 G96934	DNA-damage repair
19	66	15.6	1163	2 F84669	probable chromosom
20	65	15.4	1244	2 H86803	phosphage p13 prote
21	65	15.4	1284	2 T23744	chromosome-associ
22	64.5	15.3	205	2 A86506	GMP kinase [import
23	64.5	15.3	205	2 F72117	guanylate kinase C
24	64.5	15.3	1018	2 T40253	hypothetical prote
25	64	15.2	166	2 T43497	hypothetical prote
26	64	15.2	642	2 D81401	probable flagellar
27	63.5	15.0	417	2 E70207	antigen S1 - Lyme
28	63.5	15.0	487	2 A71407	probable Ste20-lik
29	63.5	15.0	797	2 A96232	succinoglycan bios

30	63.5	15.0	797	2 AD3054	hypothetical prote
31	63.5	15.0	1270	2 T09194	adaptor protein in
32	63	14.9	108	2 T37558	probable methyltra
33	63	14.9	672	2 T42186	conserved hypotet
34	63	14.9	862	2 A05028	rpoC protein homol
35	63	14.9	992	2 A39331	protein-tyrosine k
36	63	14.9	1000	2 S18827	Flt3 protein - mou
37	63	14.9	1033	2 S73693	MG328 homolog p01
38	63	14.9	1937	2 I38055	myosin heavy chain
39	63	14.9	2109	2 I38414	transcription fact
40	63	14.9	5005	2 F82884	hypothetical prote
41	62.5	14.8	370	1 D64550	probable membrane
42	62.5	14.8	415	2 T34156	hypothetical prote
43	62.5	14.8	509	2 T29291	hypothetical prote
44	62.5	14.8	673	2 S54182	low affinity penic
45	62.5	14.8	674	2 S54178	low affinity penic

ALIGNMENTS

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: parathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000

C:Accession: A19339; S53790; A93789; S21199; A93783; A90387; A90426; A94

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Pott

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: GB:J00301; NID:9190702; PID:AAA0215.1; PID:9190704

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid ho

A:Reference number: S53790; MUID:95225988; PMID:7710697

A:Accession: S53790

A:Molecule type: Protein

A:Residues: X'33,X'35-46:65-84;105-110 <YAM>

A:Note: Peptides generated in vitro and in vivo by meprin; peptide cleavage also

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human parathyroid hormone by a new microsequ

A:Reference number: A93169; MUID:74174967; PMID:4833316

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gaut

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylate

ation.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114,N' <OJS>

A:Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycos

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan,

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parat

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

R:Brewer Jr., H.B.; Fairwell, T.; Ronah, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal res

A:Reference number: A93783; MUID:73070429; PMID:4509319

A:Accession: A93783

A:Molecule type: protein

A;Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <RES>
 A;Note: this sequence was determined by sequenator and mass spectroscopic identification
 R;Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
 Biochemistry 14, 1842-1847, 1975
 A;Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
 A;Reference number: A90387; MUID:75146516; PMID:1125201
 A;Accession: A90387
 A;Molecule type: protein
 A;Residues: 52-75 <RES>
 R;Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
 Biochemistry 17, 5723-5729, 1978
 A;Title: Complete amino acid sequence of human parathyroid hormone.
 A;Reference number: A90426; MUID:79082855; PMID:728431
 A;Accession: A90426
 A;Molecule type: protein
 A;Residues: 61-106,'D',108-115 <RES>
 R;Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.
 in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-11
 A;Reference number: A94410
 A;Accession: A94410
 A;Molecule type: protein
 A;Residues: 75-100 <RES>
 R;Regier, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.
 Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
 A;Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human
 A;Reference number: A91660; MUID:75059220; PMID:474131
 A;Contents: annotation; synthesis of residues 32-65
 A;Note: the biologically active amino-terminal 34 residues of parathyroid hormone were
 at renal adenylate cyclase assay and with the bovine hormone's active region in the child
 R;Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel,
 Helv. Chim. Acta 56, 470-473, 1973
 A;Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
 A;Reference number: A91635; MUID:73227467; PMID:4721748
 A;Contents: annotation; synthesis of residues 32-65
 A;Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined
 into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
 R;Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
 A;Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
 A;Reference number: I38342; MUID:82150870; PMID:6950381
 A;Accession: I38342
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-115 <RES>
 A;Cross-references: EMBL:V00597; NID:937143; PIDN:CAA23843.1; PID:937144
 A;Gene: GDB:PTH
 A;Cross-references: GDB:119522; OMIM:168450
 A;Map position: 11p15.2-11p15.1
 A;Introns: 29/2
 A;Note: the first intron occurs before the initiator codon
 C;Function:
 A;Description: factor in homeostatic control of plasma calcium and phosphate; released b
 counter to calcitonin
 C;Superfamily: parathyroid hormone; parathyroid hormone homology
 C;Keywords: calcium; hormone; parathyroid gland; plasma
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-31/Domain: propeptide #status experimental <PRO>
 F;30-64/Domain: parathyroid hormone homology <PTH>
 F;32-115/Product: parathyroid hormone #status experimental <MAT>
 Query Match 98.8%; Score 417; DB 1; Length 115;
 Best Local Similarity 98.8%; Pred. No. 5.4e-37;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
 |||||
 DB 33 VSEIQLMHNGLKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 92
 QY 61 SHEKSLGEAKADVNVLTKAKSQ 83
 |||||
 DB 93 SHEKSLGEAKADVNVLTKAKSQ 115

RESULT 2

JC4202

parathyroid hormone precursor - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999

R;Accession: JC4202

Gene 160, 241-243, 1995

A;Title: Sequences of the cDNAs encoding canine parathyroid hormone-related pr

A;Reference number: JC4201; MUID:95359696; PMID:7642102

A;Accession: JC4202

A;Molecule type: mRNA

A;Residues: 1-115 <ROS>

A;Cross-references: GB:U15662; NID:9558915; PIDN:AAA82584.1; PID:9558916

C;Superfamily: parathyroid hormone; parathyroid hormone homology

C;Keywords: hormone

F;1-31/Domain: signal sequence #status predicted <SIG>

F;30-84/Domain: parathyroid hormone homology <PTH>

F;32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 86.7%; Score 366; DB 2; Length 115;
 Best Local Similarity 86.7%; Pred. No. 1.3e-31;
 Matches 72; Conservative 5; Mismatches 5; Indels 0; Gaps 0;QY 1 VSEIQLMHNGLKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
 |||||
 DB 33 VSEIQLMHNGLKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 92
 QY 61 SHEKSLGEAKADVNVLTKAKSQ 83
 |||||
 DB 93 SYOKSLGEADKADVNVLTKAKSQ 115

RESULT 3

PTB0

parathyroid hormone precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 18-Jun-1999

C;Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534

R;Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.

Gene 28, 319-329, 1984

A;Title: Isolation and complete nucleotide sequence of the gene for bovine para

A;Reference number: A24949; MUID:84262483; PMID:6086460

A;Accession: A24949

A;Molecule type: DNA

A;Residues: 1-115 <WEA>

A;Cross-references: GB:K01938

R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; PC

Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979

A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathy

A;Reference number: A93835; MUID:80056617; PMID:388425

A;Accession: A93835

A;Molecule type: DNA

A;Residues: 1-115 <KRO>

A;Cross-references: GB:J00023; NID:984; PIDN:CAA23439.1; PID:985

A;Note: the authors translated the codon GAA for residue 50 as GLY

R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.;

Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974

A;Title: The N-terminal amino-acid sequence of bovine parathyroid hormone.

A;Reference number: A93793; MUID:74142666; PMID:4522780

A;Accession: A93793

A;Molecule type: protein

A;Residues: 26-115 <HAM>

R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach,

Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970

A;Title: The amino acid sequence of bovine parathyroid hormone I.

A;Reference number: A91648; MUID:71076162; PMID:5531031

A;Accession: A91648

A;Molecule type: protein

A;Residues: 32-115 <NIA>

R;Brewer Jr., H.B.; Ronan, R.

Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970

A:Title: Bovine parathyroid hormone: amino acid sequence.
 A:Reference number: A93773; MUID:71063634; PMID:5275384
 A:Accession: A93773
 A:Molecule type: protein
 A:Residues: 32-115 <BRE>
 R:Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.; Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
 A:Title: Synthesis of a biologically active N-terminal tetraoctapeptide of parathyroid hormone.
 A:Reference number: A93776; MUID:71091588; PMID:4322265
 A:Contents: annotation; synthesis of residues 32-65
 A:Note: the synthetic peptide was active in vivo and in vitro
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D. Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 R:Weaver, C.A.; Gordon, D.F. Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
 A:Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' end of the parathyroid hormone gene.
 A:Reference number: A45975; MUID:82037785; PMID:6170060
 A:Accession: A45975
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE2>
 A:Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643
 R:Weaver, C.A.; Gordon, D.F. Mol. Cell. Endocrinol. 28, 411-424, 1982
 A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
 A:Reference number: A45976; MUID:83105964; PMID:6185374
 A:Accession: A45976
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE3>
 A:Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
 C:Genetics:
 A:Gene: PTH
 A:Introns: 29/2
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 C:Keywords: hormone
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PMAT>
 F:30-64/Domain: parathyroid hormone homology <PRO>
 F:32-115/Product: parathyroid hormone #status experimental <MAT>
 Query Match 85.1%; Score 359; DB 1; Length 115;
 Best Local Similarity 85.5%; Pred. No. 7.2e-31; Indels 0; Gaps 0;
 Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VSEIQMHNKGLHSLMSEVWLRKLLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQPMNHLGKHLSSMERVWLRKLLQDVHNFVALGASVAYRDGSSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SHQKSLGEADKADVNVLTAKPKQ 115
 RESULT 4
 PTPG
 parathyroid hormone precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 24-Apr-1984 #sequence revision 12-Apr-1996 #text_change 18-Jun-1999
 C:Accession: B26806; A90390; A90376; A01535
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H. Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone.
 A:Reference number: A26806; MUID:87316938; PMID:3628009
 A:Accession: B26806
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-115 <SCH>
 A:Cross-references: GB:X05722; GB:Y00409; NID:g1838; PIDN:CAA29193.1; PID:g1839

R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V. Biochemistry 14, 3631-3635, 1975
 A:Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.
 A:Reference number: A90390; MUID:76018954; PMID:1164500
 A:Accession: A90390
 A:Molecule type: protein
 A:Residues: 26-115 <CHU>
 R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts, J. Biochemistry 13, 1994-1999, 1974
 A:Title: The amino acid sequence of porcine parathyroid hormone.
 A:Reference number: A90376; MUID:74253317; PMID:4840833
 A:Accession: A90376
 A:Molecule type: protein
 A:Residues: 32-109 <SND>
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D. Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 C:Keywords: calcium; hormone; parathyroid gland
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Product: parathyroid hormone #status experimental <MAT>
 Query Match 84.1%; Score 355; DB 1; Length 115;
 Best Local Similarity 84.3%; Pred. No. 1.9e-30; Indels 0; Gaps 0;
 Matches 70; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VSEIQMHNKGLHSLMSEVWLRKLLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQMHNKGLHSLMSEVWLRKLLQDVHNFVALGASVAYRDGSSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SHQKSLGEADKADVNVLTAKPKQ 115
 RESULT 5
 A05091
 parathyroid hormone precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Jun-1987 #sequence revision 05-Jun-1987 #text_change 16-Jul-1999
 C:Accession: A05091; A26806
 R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F. J. Biol. Chem. 259, 3320-3329, 1984
 A:Reference number: A05091; MUID:84135846; PMID:6321505
 A:Accession: A05091
 A:Molecule type: DNA
 A:Residues: 1-115 <HEI>
 A:Cross-references: GB:K01368; NID:g206483; PIDN:AAA41979.1; PID:g206485
 A:Note: the authors translated the codon GAA for residue 87 as Asp
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H. Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone.
 A:Reference number: A26806; MUID:87316938; PMID:3628009
 A:Accession: A26806
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-115 <SCH>
 A:Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003
 C:Genetics:
 A:Introns: 29/3
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:30-64/Domain: parathyroid hormone homology <PTH>
 Query Match 73.7%; Score 311; DB 2; Length 115;
 Best Local Similarity 72.3%; Pred. No. 8.4e-26; Indels 0; Gaps 0;
 Matches 60; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 1 VSEIQMHNKGLHSLMSEVWLRKLLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60

Db 33 VSEIQLMHNKGLASVERMQWLKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 92

Qy 61 SHEKSLGEANKADVNLTKAKSQ 83

Db 93 GNSKSLGEGDKADVNLTKAKSQ 115

RESULT 6

I51851
parathyroid hormone - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I51851
R:Schmelzer, H.

Adv. Gene Technol. 21, 228-229, 1984

A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.

A:Reference number: I51851

A:Accession: I51851

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-105 <RES>

A:Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933

C:Genetics:

A:Gene: PTH

C:Superfamily: parathyroid hormone; parathyroid hormone homology

F:20-54/Domain: parathyroid hormone homology <PTH>

Query Match 71.8%; Score 303; DB 2; Length 105;

Best Local Similarity 69.9%; Pred. No. 5.3e-25;

Matches 58; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VSEIQLMHNKGLHNSMERVWLRKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 60

Db 23 ISEIQLMHNKGLASVERMQWLKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 82

Qy 61 SHEKSLGEANKADVNLTKAKSQ 83

Db 83 GNSKSLGEGDKADVNLTKAKSQ 105

RESULT 7

A34937

Parathyroid hormone precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999

C:Accession: A34937; I50411

R:Russell, J.; Sherwood, L.M.

Mol. Endocrinol. 3, 325-331, 1989

A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid

A:Reference number: A34937; MUID:89219100; PMID:2710135

A:Accession: A34937

A:Molecule type: mRNA

A:Residues: 1-119 <RUS>

A:Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768

R:Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.

J. Bone Miner. Res. 3, 689-698, 1988

A:Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.

A:Reference number: I50411; MUID:89284968; PMID:3251402

A:Accession: I50411

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-119 <KHO>

A:Cross-references: GB:M36522; NID:g212591; PIDN:AA02866.1; PID:g212592

C:Superfamily: parathyroid hormone; parathyroid hormone homology.

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-31/Domain: propeptide #status predicted <PRO>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 41.4%; Score 174.5; DB 2; Length 119;

Best Local Similarity 44.7%; Pred. No. 2.3e-11;

Matches 42; Conservative 14; Mismatches 17; Indels 21; Gaps 2;

Qy 1 VSEIQLMHNKGLHNSMERVWLRKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 60

Db 33 VSEIQLMHNKGLASVERMQWLKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 84

Qy 61 SHEKSLGEANKADVNLTKAK 81

Db 85 IRNRRLPEHLRAAVQKSDLDKAYMNVLFKTK 118

RESULT 8

G89813

DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (s.

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: G89813

R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, M.

A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.

A:Reference number: I51851

A:Accession: I51851

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-105 <RES>

A:Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933

C:Genetics:

A:Gene: PTH

C:Superfamily: parathyroid hormone; parathyroid hormone homology

F:20-54/Domain: parathyroid hormone homology <PTH>

Query Match 71.8%; Score 303; DB 2; Length 105;

Best Local Similarity 69.9%; Pred. No. 5.3e-25;

Matches 58; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VSEIQLMHNKGLHNSMERVWLRKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 60

Db 23 ISEIQLMHNKGLASVERMQWLKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 82

Qy 61 SHEKSLGEANKADVNLTKAKSQ 83

Db 83 GNSKSLGEGDKADVNLTKAKSQ 105

RESULT 9

F72408

leucine-tRNA ligase (EC 6.1.1.4) - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002

C:Accession: F72408

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.

Gartrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richard, C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from 9

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: F72408

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-824 <ARN>

A:Cross-references: GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AA035261.1; PID

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0168

C:Superfamily: leucine-tRNA ligase

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 17.2%; Score 72.5; DB 2; Length 824;

Best Local Similarity 23.3%; Pred. No. 12;

Matches 21; Conservative 25; Mismatches 25; Indels 19; Gaps 4;

Qy 4 IQLMHNKGLHNSMERVWLRKKLQDVHNFVSLGVQMAAREGSYQRTKKEENVLYD 55

Db 692 MELVNLHSLQYNSVPOEWNKLLRIVEKLTALSPFAPHLAEFFWHDLGN-----D 744

QY 56 NVLVE-----SHEKSLGEANKADVNLTAK 81

Db 745 SLVQSQWSPSYDPKALEVEVEVIAIQINGK 774

RESULT 10

138383
retinoblastoma binding protein 1, splice form I - human
N:Alternate names: retinoblastoma-associated protein 2 (mismomer)
N:Contains: retinoblastoma binding protein 1, splice form II
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: 153383; 158390; 178883; S16953; B42997
R:Rattay, A.R.; Helin, K.; Dembski, M.S.; Dyson, N.; Harlow, E.; Vuocolo, G.A.; Hanobik
Oncogene 8, 3149-3156, 1993
A:Title: Characterization of the retinoblastoma binding proteins RBP1 and RBP2.
A:Reference number: 158383; MUID:94020941; PMID:8414517
A:Accession: 158383
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1257 <FAT>
A:Cross-references: GB:S66427; MID:9435775; PIDN:AAB28543.1; PID:94335776
R:Otterson, G.A.; Kratzke, R.A.; Lin, A.Y.; Johnston, P.G.; Kaye, F.J.
Oncogene 8, 949-957, 1993
A:Title: Alternative splicing of the RBP1 gene clusters in an internal exon that encodes
A:Reference number: 158390; MUID:93205410; PMID:8455946
A:Accession: 158390
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1257 <OTT1>
A:Cross-references: GB:S57153; MID:9298681; PIDN:AAB25833.1; PID:9298682
A:Accession: 178883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1120, 1175-1257 <OTT2>
A:Cross-references: GB:S57160; MID:9298683; PIDN:AAB25834.1; PID:9298684
R:Deleo-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.
Nature 352, 251-254, 1991
A:Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene pro
A:Reference number: S16953; MUID:91312450; PMID:1857421
A:Accession: S16953
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 855-1177, 'S', 1179-1195, 'SENIICL' <DEF>
R:Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; Decaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.
Cell 70, 351-364, 1992
A:Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F
A:Reference number: A42997; MUID:92346721; PMID:1638635
A:Accession: B42997
A:Molecule type: mRNA
A:Residues: 'NMTMKL', 510-617, 'R', 619-1257 <RAE>
A:Experimental source: Akata cells
A:Note: the cited GenBank accession number, M95577, is apparently a misprint and does no
C:Genetics:
A:Gene: GDB:RBP1
A:Cross-references: GDB:120340; OMIM:180260
A:Map position: 3q21-3q22
C:Superfamily: human retinoblastoma binding protein 1
C:Keywords: alternative splicing
F:1-1257/Product: retinoblastoma binding protein 1, splice form I #status predicted <SP
F:1-1120, 1175-1257/Product: retinoblastoma binding protein 1, splice form II #status pre

Query Match

Best Local Similarity 26.88; Pred. No. 23;

Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;

QY 13 HLMSEMERVEWLRKLDVHN-FVALGAPLAPRAGSORPRKKEDNVLSHEKSLGEANK 71

Db 1179 NMNSTERISFLQELQIRKYKYSKSEVATIDRRRLKKDKREV---SHAGASMSSAS 1235

QY 72 ADVNVLTKAKS 82

Db 1236 SDTGMSPSSSS 1246

RESULT 11

T44010
villon protein [imported] - human herpesvirus 6
C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44010; T44197
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa,
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variant
A:Reference number: 227332; MUID:99412319; PMID:10482554
A:Accession: T44010
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <ISE>
A:Cross-references: EMBL:AB021505; MID:94995977; PIDN:BAA78271.1; PID:94996038
A:Experimental source: strain HST; pop. variant B
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett,
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison wit
A:Reference number: 227334; MUID:99412318; PMID:10482553
A:Accession: T44197
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AAB06348.1
A:Experimental source: strain Z29; variant B
C:Genetics:
A:Gene: US0
C:Superfamily: varicella-zoster virus gene 34 protein

Query Match 16.5%; Score 69.5; DB 2; Length 555;

Best Local Similarity 35.4%; Pred. No. 16;

Matches 23; Conservative 10; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKKLDVHNFVALGAPLAPRAGSORPRKKEDNVLSHEKSLGEA----NKADVNVL 78

Db 42 LREKIDQGRKDLRLMKLTDLALQKRWKSDVL-NSHLKATIEDALLFINDGEVNVET 100

QY 79 KAKSQ 83

Db 101 KADTQ 105

RESULT 12

B70356
chromosome assembly protein homolog - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
C:Accession: B70356
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: B70356
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1156 <AQF>
A:Cross-references: GB:AE000699; MID:92983238; PIDN:AAC06839.1; PID:92983243; GB:
A:Experimental source: strain VF5
C:Genetics:
A:Gene: xcpC
C:Superfamily: chromosome segregation protein SMCI

Query Match

Best Local Similarity 29.08; Pred. No. 61;

Matches 27; Conservative 16; Mismatches 25; Indels 25; Gaps 4;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 59.4627 Seconds
(without alignments)
221.556 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHLNGLKHLMSERV.....KSLGEANKADVNLTKAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	422	100.0	83	24	Human parathyroid
2	422	100.0	84	21	Amino acid sequenc
3	422	100.0	84	24	Human full length
4	418	99.1	82	21	Amino acid sequenc
5	418	99.1	82	24	Human parathyroid
6	417	98.8	84	13	Parathyroid hormon
7	417	98.8	84	13	Human PTH encoded
8	417	98.8	84	14	Human parathyroid
9	417	98.8	84	17	Human parathyroid

10	417	98.8	84	17	Target peptide (PT
11	417	98.8	84	18	Human parathyroid
12	417	98.8	84	20	Human parathyroid
13	417	98.8	84	22	Parathyroid hormon
14	417	98.8	84	23	Human parathyroxin
15	417	98.8	84	23	Human parathyroid
16	417	98.8	84	23	Human PTH peptide
17	417	98.8	84	23	Salmon calcitonin
18	417	98.8	84	23	Parathyroid hormon
19	417	98.8	84	24	Human parathyroid
20	417	98.8	84	24	Human bioactive pa
21	417	98.8	115	5	Protein sequence i
22	417	98.8	115	9	Sequence of human
23	417	98.8	115	9	Human prepro-PTH.
24	417	98.8	115	16	Oxidation resistan
25	417	98.8	115	16	Oxidation resistan
26	417	98.8	115	16	Leu18 hPTH mutain.
27	417	98.8	115	16	Stability-enhanced
28	417	98.8	115	16	Cys35 hPTH mutain.
29	417	98.8	115	16	Stability-enhanced
30	417	98.8	115	16	Human parathyroid
31	417	98.8	115	16	Human PTH(1-84) pe
32	417	98.8	115	16	Oxidation resistan
33	417	98.8	115	16	Oxidation resistan
34	417	98.8	115	16	Stability-enhanced
35	417	98.8	115	16	Sequence of varian
36	417	98.8	115	16	Sequence of varian
37	417	98.8	115	16	Oxidation resistan
38	417	98.8	115	16	Oxidation resistan
39	417	98.8	115	16	Stability-enhanced
40	417	98.8	115	16	Sequence of varian
41	417	98.8	115	16	Sequence of varian
42	417	98.8	115	16	Oxidation resistan
43	417	98.8	115	16	Oxidation resistan
44	417	98.8	115	16	Stability-enhanced
45	417	98.8	115	16	Sequence of varian

ALIGNMENTS

RESULT 1
ABG74230
ID ABG74230 standard; peptide; 83 AA.
XX AC ABG74230;
XX AC
XX 16-APR-2003 (first entry)
XX
XX Human parathyroid hormone-based CIP, PTH2-84.
DE
XX Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
XX hypercalcaemia; osteosarcoma; extracellular calcium; PTH2-84.
XX
XX Homo sapiens.
OS
XX US2002160945-A1.
XX
XX 31-OCT-2002.
XX
XX 10-AUG-2001; 2001US-0928047.
XX
XX 10-AUG-2000; 2000US-224446P.
XX
XX (CANTOR) CANTOR T L.
XX
XX Cantor TL;
XX
XX WPI; 2003-209227/20.
XX
XX Treating a patient having osteoporosis and is being administered
PT cyclase activating parathyroid hormone or its analogue comprises

PT administering a cyclase inhibiting parathyroid hormone peptide -
PS Claim 1; Page 3; 8pp; English.
XX The invention relates to treating a patient having osteoporosis
CC comprising administering a cyclase inhibiting parathyroid hormone peptide
CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
CC hormone (PTH, which regulates extracellular calcium levels) antagonist
CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
CC the patient resulting from the administration of CAP. The peptide
CC comprises PTH2-84, PTH3-84, PTH3-84 and PTH28-84 (appearing as ABG74230
CC -ABG74233). The present sequence is the CIP PTH2-84.
XX
SQ Sequence 83 AA;

Query Match 100.0%; Score 422; DB 24; Length 83;
Best Local Similarity 100.0%; Pred. No. 5.6e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
Db 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
Db 61 SHEKSLGEANKADVNLTKAKSQ 83

RESULT 2
AAB07464
ID AAB07464 standard; protein; 84 AA.
AC AAB07464;
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of human parathyroid hormone.
XX
KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS Homo sapiens.
XX
PN WO2000042437-A1.
XX
PD 20-JUL-2000.
XX
PF 13-JAN-2000; 2000WO-US00855.
XX
PR 14-JAN-1999; 99US-0231422.
XX
PR 26-JUN-1999; 99US-0344639.
XX
PA (SCAN-) SCANTIBODIES LAB INC.
XX
DR WPI; 2000-476147/41.
XX
PT Differentiating between normal parathyroid function and
PT hyperparathyroidism comprises determining and comparing whole
PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT and/or total parathyroid hormone levels.
XX
PS Disclosure; Fig 1; 46pp; English.
XX
CC The present sequence represents a human parathyroid hormone (PTH).
CC Fragments of PTH function as PTH antagonists. The specification
CC describes a method for differentiating between a person having
CC substantially normal parathyroid function and having hyperparathyroidism.
CC The method comprises determining and comparing at least two of the
CC following parameters: whole parathyroid hormone level, parathyroid
CC hormone inhibitory peptide fragment level and total parathyroid hormone
CC level. The method is used for monitoring (treatments of) parathyroid
CC related bone disease and the effects of therapeutic treatment for
CC hyperparathyroidism.
XX

SQ Sequence 84 AA;

Query Match 100.0%; Score 422; DB 21; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
Db 2 VSEIQLMHNGLKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
Db 62 SHEKSLGEANKADVNLTKAKSQ 84

RESULT 3
ABG74234
ID ABG74234 standard; peptide; 84 AA.
XX
AC ABG74234;
XX
DT 16-APR-2003 (first entry)
XX
DE Human full length parathyroid hormone.
XX
KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
KW hypercalcaemia; osteosarcoma; extracellular calcium.
XX
OS Homo sapiens.
XX
PN US2002160945-A1.
XX
PD 31-OCT-2002.
XX
PF 10-AUG-2001; 2001US-0928047.
XX
PR 10-AUG-2000; 2000US-224446P.
XX
PA (CANT/) CANTOR T L.
XX
PI Cantor TL;
XX
DR WPI; 2003-209227/20.
XX
PT Treating a patient having osteoporosis and is being administered
PT cyclase activating parathyroid hormone or its analogue comprises
PT administering a cyclase inhibiting parathyroid hormone peptide -
PS Disclosure; Fig 1; 8pp; English.
XX
CC The invention relates to treating a patient having osteoporosis
CC comprising administering a cyclase inhibiting parathyroid hormone peptide
CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
CC hormone (PTH, which regulates extracellular calcium levels) antagonist
CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
CC the patient resulting from the administration of CAP. The peptide
CC comprises PTH2-84, PTH3-84, PTH3-84 and PTH28-84 (appearing as ABG74230
CC -ABG74233). The present sequence is full length human PTH, the sequence
CC upon which the CIP peptides are based.
XX
SQ Sequence 84 AA;

Query Match 100.0%; Score 422; DB 24; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
Db 2 VSEIQLMHNGLKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
XXXXXXXXXXXXXXXXXXXXXXXXXXXX

Parathyroid hormone; PTH; cyclase activating parathyroid hormone; CIP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH34-84.	
Homo sapiens.	
US2002160945-A1.	
31-OCT-2002.	
10-AUG-2001; 2001US-0928047.	
10-AUG-2000; 2000US-224446P.	
(CANT/)	CANTOR T L.
	Cantor TL;
WPI; 2003-209227/20.	
Treating a patient having osteoporosis and its being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide -	
Claim 1; Page 3; 8pp; English.	
The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH, which regulates extracellular calcium levels) antagonistic activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74233). The present sequence is the CIP PTH34-84.	
Sequence	82 AA;
Query Match	99.1%; Score 418; DB 24; Length 82;
Best Local Similarity	100.0%; Pred. No. 1.6e-41;
Matches	82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2 SEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVV
Db	1 SEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVV
QY	62 HEKSLGEANKADVNLTKAKSQ 83
Db	61 HEKSLGEANKADVNLTKAKSQ 82
RESULT 6	
AAR23790	
ID	AAR23790 standard; Protein; 84 AA.
XX	
AC	AAR23790;
XX	
DT	03-NOV-1992 (first entry)
XX	
DE	Parathyroid hormone gene product.
XX	
KW	hPTH; hypoparathyroidism; osteoporosis.
XX	
OS	Synthetic.
XX	
FN	EP483509-A.
XX	
PD	06-MAY-1992.
XX	
PF	25-SEP-1991; 91EP-0116281.
XX	
PR	28-SEP-1990; 90JP-0257491.
XX	
PR	20-MAR-1991; 91JP-0056434.
XX	

PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Oshikazu Y, Yamada T;
 XX
 DR WPI; 1992-152248/19.
 DR N-PSDB; AAQ24478.
 XX
 PT Synthetic gene encoding human parathyroid hormone - formed by
 PT ligating oligo-nucleotide(s) and expressed at high yield in E
 PT coli
 XX
 PS Disclosure; Page 21; 33pp; English.
 XX
 CC The human parathyroid hormone (hPTH) sequence given is the product of
 CC a synthetic gene which corresponds to the amino acid sequence of hPTH.
 CC The DNA sequence was produced by enzymatically ligating
 CC oligodeoxynucleotides. hPTH is an important regulator of calcium
 CC metabolism and has clinical applicns. to diseases such as
 CC hypoparathyroidism and osteoporosis. This hPTH can be used as a
 CC therapeutic agent or to study the biological role of hPTH in vivo.
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 13; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 QY 61 SHEKSLGEANKADVNLTKAKSQ 83
 DB 62 SHEKSLGEADKADVNLTKAKSQ 84
 RESULT 7
 AAR25571
 ID AAR25571 standard; Protein; 84 AA.
 XX
 AC AAR25571;
 XX
 DT 25-MAR-2003 (updated)
 DT 13-JAN-1993 (first entry)
 XX
 DE Human PTH encoded by px.
 XX
 KW Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
 KW resistance.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /note= "see CC"
 FT Misc-difference 18 /note= "see CC"
 FT
 XX
 PN WO9211286-A1.
 XX
 PD 09-JUL-1992.
 XX
 PF 18-DEC-1991; 91WO-CA00451.
 XX
 PR 21-DEC-1990; 90US-0630969.
 PR 13-DEC-1991; 91US-0806271.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzatto RP, Kronis KA;
 XX
 DR WPI; 1992-250028/30.
 XX

DR N-PSDB; AAQ26498.
 XX
 PT New oxidn. resistant variants of parathyroid hormone - used for
 PT treating osteoporosis, psoriasis and cardiovascular disorders
 XX
 PS Disclosure; Fig 1; 40pp; English.
 XX
 CC Variants of PTH exhibiting PTH activity and reduced sensitivity
 CC to oxidation are obtained by replacing at least one Met residue in
 CC PTH (positions 8 and 18) with a genetically encoded amino acid,
 CC other than Met and Cys.
 CC The Met amino acids are indicated in the Features Table.
 CC The variant may be obtd. using recombinant technique, and may be
 CC used for treating osteoporosis, other bone-related disorders,
 CC psoriasis and cardiovascular disorders.
 CC Human PTH refers to the mature form of the hormone, which consists
 CC of 84 amino acids arranged in the sequence reported by Kimura et al,
 CC 1983, Biochem. Biophys. Res. Comm., 114(2):493.
 CC Examples of variants are given in AAR28845-48 and AAR29561-69.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 13; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 QY 61 SHEKSLGEANKADVNLTKAKSQ 83
 DB 62 SHEKSLGEADKADVNLTKAKSQ 84
 RESULT 8
 AAR42067
 ID AAR42067 standard; Protein; 84 AA.
 XX
 AC AAR42067;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-MAY-1994 (first entry)
 XX
 DE Human parathyroid hormone.
 XX
 KW PTH; hPTH; stability-enhanced; mutant; resistance; proteolytic;
 KW enzymes; osteoporosis; bone-related disorders.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 25...27
 FT /note= "ArgLysLys which may be mutated"
 XX
 PN WO9320203-A2.
 XX
 PD 14-OCT-1993.
 XX
 PF 31-MAR-1993; 93WO-CA00136.
 XX
 PR 03-APR-1992; 92US-0853014.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzatto RP, Kronis KA;
 XX
 DR WPI; 1993-336911/42.
 DR N-PSDB; AAQ49955.
 XX

PT New parathyroid hormone variants - having aminoacid replacements
 PT at positions 25 to 27 to enhance resistance to proteolytic
 XX enzymes
 PS Disclosure: Fig 2; 44pp; English.
 XX The sequence is that of human parathyroid hormone (hPTH) which
 CC may be mutated in the region Arg25Lys26Lys27 to provide variants
 CC with enhanced stability in the presence of proteolytic enzymes
 CC such as trypsin.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 14; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 OY 61 SHEKSLGEANKADVNVLTKAKSQ 83
 DB 62 SHEKSLGEADKADVNVLTKAKSQ 84
 RESULT 9
 ID AAW29420 standard; protein; 84 AA.
 AC AAW29420;
 XX
 DT 25-MAR-2003 (updated)
 DT 24-FEB-1998 (first entry)
 XX
 DE Human parathyroid hormone.
 XX
 KW Parathyroid hormone; PTH; osteoporosis; inhalation; pulmonary;
 KW bone formation.
 XX
 OS Homo sapiens.
 XX
 PN WO9619206-A1.
 XX
 PD 27-JUN-1996.
 XX
 PF 08-DEC-1995; 95WO-SE01475.
 XX
 PR 12-JUL-1995; 95SE-0002576.
 PR 22-DEC-1994; 94SE-0004449.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Baectstroem K, Wallmark B;
 XX
 DR WPI; 1996-309285/31.
 XX
 PT Composition for administration by inhalation to treat osteoporosis
 PT and stimulate bone formation - comprises parathyroid hormone in form
 PT of dry powder mainly of particle size below 10 microns
 XX
 PS Claim 9; Pages 15-16; 25pp; English.
 XX
 CC The present sequence represents human parathyroid hormone which is used
 CC in a new therapeutic preparation for the treatment of osteoporosis.
 CC The active substance is in the form of a dry powder suitable for
 CC inhalation, in which at least 50% of the dry powder consists of particles
 CC of up to 10 microns in diameter or agglomerates of such particles.
 CC Pulmonary administration of the parathyroid hormone is effective in the
 CC stimulation of bone formation.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 CC

XX Sequence 84 AA;
 SQ
 Query Match 98.8%; Score 417; DB 17; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 OY 61 SHEKSLGEANKADVNVLTKAKSQ 83
 DB 62 SHEKSLGEADKADVNVLTKAKSQ 84
 RESULT 10
 ID AAR98954 standard; peptide; 84 AA.
 XX
 AC AAR98954;
 XX
 DT 15-JAN-1997 (first entry)
 XX
 DE Target peptide (PTH(1-84)) used in fusion protein construct.
 XX
 KW Fusion protein construct; isolation; purification;
 KW growth hormone releasing factor; glucagon-like peptide 1;
 KW parathyroid hormone; inclusion body; carbonic anhydrase.
 XX
 OS Synthetic.
 XX
 PN WO9617942-A1.
 XX
 PD 13-JUN-1996.
 XX
 PF 07-DEC-1995; 95WO-US15800.
 XX
 PR 07-DEC-1994; 94US-0350530.
 XX
 PA (BION-) BIONEERASKA INC.
 XX
 PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;
 PI Partridge BE, Stout JS, Wagner FW;
 XX
 DR WPI; 1996-287186/29.
 XX
 PT Isolation and purific of peptide(s) from fusion protein constructs
 PT - which include a carbonic anhydrase and a variable fused
 PT polypeptide
 XX
 PS Claim 58; Page 49; 67pp; English.
 XX
 CC A new method for the isolation and/or purification of a recombinant
 CC peptide employs a fusion protein construct (FPC) comprising a
 CC carbonic anhydrase and a variable fused polypeptide containing a
 CC target peptide. The method comprises precipitating either the FPC or
 CC a fragment of the FPC including the carbonic anhydrase. An
 CC alternative method of producing the peptide comprises expressing the
 CC FPC as part of an inclusion body. The target peptides of the FPC are
 CC derived from growth hormone releasing factor (GRF), glucagon-like
 CC peptide 1 (GluP1) or parathyroid hormone (PTH). This sequence
 CC corresponds to amino acids 1-84 of PTH.
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 17; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNLTAKSQ 83
 DB 62 SHEKSLGEADKADVNLTAKSQ 84

RESULT 11

AAW25687
 ID AAW25687 standard; Peptide; 84 AA.

XX AC AAW25687;

DT 14-APR-1998 (first entry)

DE Human parathyroid hormone peptide hPTH (residues 1-84).

KW Kex2 protease; derivative; cleave; yeast; enzyme; chimeric protein;
 KW human; parathyroid hormone peptide; hPTH.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Cleavage-site 43..44 /note= "cleaved by Kex2 protease"

FT Cleavage-site 51..52 /note= "cleaved by Kex2 protease"

FT EP794254-A2.

PN 10-SEP-1997.

PD 04-MAR-1997; 97EP-0301429.

PR 16-DEC-1996; 96JP-0352580.

PR 04-MAR-1996; 96JP-0073217.

XX (SUNR) SONTORY LTD.

PI Magota K, Masuda T, Suzuki Y, Yabuta M;

XX WPI; 1997-437479/41.

XX Secreted forms of Kex2 protease - useful for cleaving chimeric
 PT proteins

PS Disclosure; page 25; 82pp; English.

XX This is the human parathyroid hormone peptide hPTH (residues 1-84). This
 CC is used in the construction of a chimeric protein betaGal-139S(FM)PPH84.
 CC The enzyme Kex2 protease can be used for excision of a desired protein
 CC from a chimeric protein comprising the desired protein and an Arg-Arg,
 CC Lys-Arg or Pro-Arg sequence adjacent to the N terminus of the desired
 CC protein. It can be specifically used for cleaving this human parathyroid
 CC hormone peptide hPTH(1-84) or peptide hPTH(1-34) from chimeric proteins
 CC such as the beta Gal-139S(FM)PPH84 or CATPH34. Derivatives of Kex2
 CC protease, and especially kex2-660 can also cleave such chimeric proteins
 CC with high specificity and efficiency even in the absence of urea.

XX Sequence 84 AA;

Query Match 98.8%; Score 417; DB 18; Length 84;

Best Local Similarity 98.8%; Pred. No. 2.2e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSETQLMHNLGKHLNSMERVETLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60

DB 2 VSETQLMHNLGKHLNSMERVETLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNLTAKSQ 83

DB 62 SHEKSLGEADKADVNLTAKSQ 84

RESULT 12

AAW2577

ID AAY02577 standard; protein; 84 AA.

XX AC AAY02577;

XX 16-JUL-1999 (first entry)

DE Human parathyroid hormone (hPTH) protein.

KW Human parathyroid hormone; hPTH; bone mass;
 KW 3-(substituted phenoxy)benzo(b)thiophene compound;
 KW bone loss treatment; osteoporosis.

XX Homo sapiens.

XX WO9918945-A1.

XX 22-APR-1999.

XX 05-OCT-1998; 98WO-US20848.

XX 14-OCT-1997; 97US-0061800.

XX (ELIL) LILLY & CO ELI.

XX Sato M;

XX WPI; 1999-287871/24.

XX Method of building bone mass by co-administration of a parathyroid
 PT hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound

XX Claim 5; Page 38; 48pp; English.

XX The present sequence represents human parathyroid hormone (hPTH). It,
 CC and its fragments, are used in the method of the invention. The
 CC specification describes a method for building bone mass, comprising
 CC coadministration of a parathyroid hormone with a 3-(substituted
 CC phenoxy)benzo(b)thiophene compound. The method is used for treatment
 CC of bone loss, e.g. in osteoporosis.

XX Sequence 84 AA;

Query Match 98.8%; Score 417; DB 20; Length 84;

Best Local Similarity 98.8%; Pred. No. 2.2e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSETQLMHNLGKHLNSMERVETLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60

DB 2 VSETQLMHNLGKHLNSMERVETLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNLTAKSQ 83

DB 62 SHEKSLGEADKADVNLTAKSQ 84

RESULT 13

AAB91082

ID AAB91082 standard; Peptide; 84 AA.

XX AC AAB91082;

XX 22-JUN-2001 (first entry)

DE Parathyroid hormone (PTH) related peptide SEQ ID NO:256.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.
 XX 23-NOV-2000.
 XX 17-MAY-2000; 2000WO-US13576.
 XX 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX (CONJ-) CONJUCHEM INC.
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX Disclosure; Page 274-275; 733pp; English.
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX Sequence 84 AA;
 SQ
 Query Match 98.8%; Score 417; DB 22; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
 Db 2 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61
 OY 61 SHEKSLGEANKADVNLTKAKSQ 83
 Db 62 SHEKSLGEANKADVNLTKAKSQ 84
 RESULT 14
 ABG71472
 ID ABG71472 standard; Protein; 84 AA.
 XX AC ABG71472;
 XX DT 28-FEB-2003 (first entry)
 XX DE Human parathyroxin (hPTH) related protein.
 XX KW Parathyroxin; hPTH.
 XX OS Unidentified.
 XX CN153115-A.
 XX 12-JUN-2002.

XX 13-NOV-2000; 2000CN-0133573.
 XX 13-NOV-2000; 2000CN-0133573.
 XX (MEIB/) MEI B.
 XX Huang X, You Z, Li S;
 XX WPI; 2002-751425/82.
 XX N-PSDB; ABS57477.
 XX Synthesis and expression of recombinant human parathyroxin gene
 PT Disclosure; Fig 1; 16pp; Chinese.
 XX The invention relates to a DNA sequence containing a fragment of the
 CC human parathyroxin (hPTH) gene. The invention also relates to splicing
 CC artificially synthesised oligodeoxynucleotide chains by PCR and preparing
 CC fusion or non-fusion expressed engineering bacteria of recombination
 CC protein hPTH through integrating the gene in different expression
 CC carriers. This sequence represents a human parathyroxin related protein.
 XX Sequence 84 AA;
 SQ
 Query Match 98.8%; Score 417; DB 23; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
 Db 2 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61
 OY 61 SHEKSLGEANKADVNLTKAKSQ 83
 Db 62 SHEKSLGEANKADVNLTKAKSQ 84
 RESULT 15
 AAE23726
 ID AAE23726 standard; peptide; 84 AA.
 XX AC AAE23726;
 XX DT 10-SEP-2002 (first entry)
 XX DE Human parathyroid hormone (hPTH) peptide (1-84).
 XX KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.
 XX OS Homo sapiens.
 XX WO200228420-A2.
 XX 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US31082.
 XX 06-OCT-2000; 2000US-238134P.
 XX (HOLI/) HOLICK M F.
 XX Holick MF;
 XX WPI; 2002-452304/48.
 XX N-PSDB; AAD37995.
 XX Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein.

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Claim 5; Fig 18; 56pp; English.

The invention relates to a method for regulating proliferation or enhancing differentiation of mammalian skin or hair cell. The method involves administering nucleic acids encoding peptides derived from N-terminal region of human parathyroid hormone (hPTH) or hPTH-related peptide (PTHrP). The method is used for inhibiting hyperproliferative skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic keratosis, skin cancer, for inhibiting hair growth or preventing hair regrowth. It is useful for stimulating cell growth, rejuvenating aged skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound healing, stimulating hair growth, maintaining hair growth, treating or preventing female or male pattern baldness, for treating chemotherapy induced alopecia and also for stimulating epidermal cell growth or hair follicle cell growth. The method is also used in gene therapy. The present sequence is hPTH peptide.

Sequence 84 AA:

Query Match 98.8%; Score 417; DB 23; Length 84;

Best Local Similarity 98.8%; Pred. No. 2.2e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VSEIQLMHNGLKHLNSMERVEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60

Db 2 VSEIQLMHNGLKHLNSMERVEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61

OY 61 SHEKSLGEANKADVNLTKAKSQ 83

Db 62 SHEKSLGEANKADVNLTKAKSQ 84

Search completed: October 9, 2003, 08:10:45
Job time : 59.9627 secs

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OM protein - protein search, using sw model

Run on: October -9, 2003, 08:08:56 ; Search time 16.1045 Seconds
(without alignments)
242.368 Million cell updates/sec

Title: US-09-928-048a-4
Perfect score: 422
Sequence: 1 VSEIQMLNGLKHLNSMERV.....KSLGEANKADVNVLTAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	98.8	115	1	PTHY_HUMAN
2	410	97.2	115	1	PTHY_MACFA
3	366	86.7	115	1	PTHY_CANFA
4	359	85.1	115	1	PTHY_BOVIN
5	355	84.1	115	1	PTHY_PIG
6	311	73.7	115	1	PTHY_RAT
7	174.5	41.4	119	1	PTHY_CHICK
8	72.5	17.2	824	1	SVL_THEMA
9	72	17.1	1257	1	RBL1_HUMAN
10	69.5	16.5	555	1	UL25_HSV62
11	68	16.1	606	1	GLMS_FUSNN
12	67	15.9	443	1	HSJL_VIBCH
13	66.5	15.8	378	1	UL25_HSV66
14	66.5	15.8	555	1	UL25_HSV60
15	66	15.6	396	1	DPO4_CLOAB
16	65	15.4	1244	1	MX11_CAEEL
17	64.5	15.3	205	1	KGA_CHLPN
18	64.5	15.3	668	1	SGI_PIG
19	64	15.2	642	1	FLTD_CAMJE
20	63.5	15.0	1270	1	ITN1_XENLA
21	63	14.9	992	1	FLT3_MOUSE
22	63	14.9	1033	1	Y328_MYCPN
23	63	14.9	1388	1	PROD_TOBAC
24	63	14.9	1937	1	MYH8_HUMAN
25	62.5	14.8	370	1	YAA4_HELPY
26	62.5	14.8	632	1	DNAA_ACTAC
27	62.5	14.8	1658	1	ITN2_MOUSE
28	62	14.7	300	1	YSDO_ECOLI
29	62	14.7	1041	1	DD16_HUMAN
30	61.5	14.6	366	1	YE05_HAEIN
31	61	14.5	429	1	DPD2_ORYSA
32	61	14.5	910	1	HUL5_YEAST
33	60.5	14.3	942	1	PKL1_HUMAN

ALIGNMENTS

RESULT 1

ID	PTHY_HUMAN	STANDARD;	PRT;	115 AA.
AC	P01270;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."			
RT	hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83169834; PubMed=6220408;			
RA	Vasicek T.J., McDevitt B.E., Freeman M.W., Pennick B.J.,			
RA	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RT	"Nucleotide sequence of the human parathyroid hormone gene."			
RT	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RN	[3]			
RP	SEQUENCE OF 26-37.			
RX	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new			
RT	microsequencing approach."			
RL	Nature 249:155-157(1974).			
RN	[4]			
RP	SEQUENCE OF 32-68.			
RX	MEDLINE=74111656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RA	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RT	"The amino-acid sequence of the amino-terminal 37 residues of human			
RT	parathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RN	[5]			
RP	SEQUENCE OF 61-83 AND 84-115.			
RX	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RA	Potts J.T. Jr.;			
RT	"Complete amino acid sequence of human parathyroid hormone."			
RL	Biochemistry 17:5723-5729(1978).			
RN	[6]			
RP	SEQUENCE OF 75-100.			
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RA	O'Riordan J.L.H., Potts J.T. Jr.;			
RL	(In) Talmadge R.V., Owen M., Parsons J.A. (eds.);			
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,			
RL	Amsterdam (1975).			

015811 homo sapien
P06618 pseudomonas
P35841 desulfovibr
P33175 mus musculu
012840 homo sapien
P02562 cryptolagus
P94974 mycobacteri
Q90339 cyprinus ca
Q28641 cryptolagus
P02565 gallus gall
015020 homo sapien
O31211 staphylococ

(7) REVISIONS.
 RX MEDLINE-75146516; PubMed=1125201;
 RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "A re-investigation of the amino-terminal sequence of human
 parathyroid hormone."
 RL Biochemistry 14:1842-1847(1975).
 RN (8)
 RX SYNTHESIS OF 32-65.
 RA MEDLINE-75059220; PubMed=4474131;
 RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
 RA Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "Solid-phase synthesis of the biologically active N-terminal 1-34
 peptide of human parathyroid hormone."
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
 RN (9)
 RX SYNTHESIS OF 32-65.
 RA MEDLINE-7327467; PubMed=4721748;
 RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
 RA Knicker B., Rittel W., Sieber P.;
 RT "Synthesis of sequence 1-34 of human parathyroid hormone."
 RL Helv. Chim. Acta 56:470-473(1973).
 RN (10)
 RX STRUCTURE BY NMR OF 32-65.
 RA MEDLINE-91289748; PubMed=2069952;
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
 RT "Investigation of the solution structure of the human parathyroid
 hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
 and molecular dynamics calculations."
 RL Biochemistry 30:6936-6942(1991).
 RN (11)
 RX STRUCTURE BY NMR OF 32-65.
 RA MEDLINE-93345518; PubMed=8344299;
 RA Barden J.A., Cuthbertson R.M.;
 RT "Stabilized NMR structure of human parathyroid hormone(1-34).";
 RL Eur. J. Biochem. 215:315-321(1993).
 RN (12)
 RX STRUCTURE BY NMR OF 32-68.
 RA MEDLINE-95318084; PubMed=7797503;
 RA Marx U.C., Adermann K., Bayer P., Adermann K., Eychart A.,
 RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
 RA Roesch P.;
 RT "Structure of human parathyroid hormone 1-37 in solution."
 RL J. Biol. Chem. 270:15194-15202(1995).
 RN (13)
 RX STRUCTURE BY NMR OF 32-70.
 RA MEDLINE-20090619; PubMed=10623601;
 RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
 RT "Solution structures of human parathyroid hormone fragments
 hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
 bPTH(1-37).";
 RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
 RN (14)
 RX VARIANT ARG-18.
 RA MEDLINE-91009811; PubMed=2212001;
 RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
 RA Kronenberg H.M.;
 RT "Mutation of the signal peptide-encoding region of the
 preproparathyroid hormone gene in familial isolated
 hypoparathyroidism."
 RL J. Clin. Invest. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: Defects in PTH are a cause of familial isolated
 hypoparathyroidism (FIH) [MIM:146200].
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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 CC -----
 CC ENBL; J00301; AAA60215.1; --
 DR EMBL; V00597; CAA23843.1; --
 DR EMBL; A29146; CAA01956.1; --
 DR PIR; A19339; PTHU.
 DR PDB; 1HPH; 10-JUL-95.
 DR PDB; 1HTH; 15-OCT-97.
 DR PDB; 1ZNA; 12-MAR-97.
 DR PDB; 1ZNB; 12-MAR-97.
 DR PDB; 1ZWD; 12-MAR-97.
 DR PDB; 1ZWE; 12-MAR-97.
 DR PDB; 1ZWF; 16-JUN-97.
 DR PDB; 1ZWG; 16-JUN-97.
 DR PDB; 1BWX; 14-JAN-00.
 DR PDB; 1HPY; 14-JAN-00.
 DR PDB; 1ETI; 06-SEP-00.
 DR PDB; 1ETZ; 06-SEP-00.
 DR PDB; 1FVJ; 31-DEC-02.
 DR Genew; HGNC:9606; PTH.
 DR MIM; 168450; --
 DR MIM; 146200; --
 DR GO; GO:0008492; F:AMP generating peptide activity; TAS.
 DR GO; GO:0005180; F:peptide hormone; TAS.
 DR GO; GO:0007367; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.
 DR GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR001415; Parathyrd_hrm.
 DR InterPro; IPR003625; Pthyrdorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyrdorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 DR Hormone; Signal; Disease mutation; 3D-structure.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT
 FT CONFLICT 107 107
 FT HELIX 36 41
 FT TURN 42 43
 FT HELIX 49 63
 FT TURN 64 66
 FT
 SQ SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;
 Query Match 98.8%; Score 417; DB 1; Length 115;
 Best Local Similarity 98.8%; Pred. No. 9.4e-39;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNLMERVEWLRKKLDVHNFVALGAPLAPRDSQRRPKEDNVLYE 60
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 33 VSEIQLMHNGLKHLNLMERVEWLRKKLDVHNFVALGAPLAPRDSQRRPKEDNVLYE 92
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 93 SHEKSLGEANKADVNVLTAKSQ 115
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 2
 PTH_MACFA STANDARD; PRT; 115 AA.
 ID PTH_MACFA
 AC Q9YH35;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 GN PTH
 OS Parathyroid hormone precursor (Parathyrin) (PTH).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

CC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Malaivijitnond S., Takenaka O.;
 RT "Nucleotide sequences of parathyroid gene in five species of macaque of Thailand.";
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
 CC - FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC - SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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 CC -----
 DR EMBL: AF130257; AAD42777.1;
 DR HSSP: P01270; LHPY.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR Pfam: P01279; Pthyrhorm_sub.
 DR ProDom: PD010687; Pthyrhorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;
 Query Match 97.2%; Score 410; DB 1; Length 115;
 Best Local Similarity 95.2%; Pred. No. 5.5e-38;
 Matches 79; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNLMERVWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQLMHNGLKHLNLMERVWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SHEKSLGEANKADVNVLTAKSQ 115
 Query Match 97.2%; Score 410; DB 1; Length 115;
 Best Local Similarity 95.2%; Pred. No. 5.5e-38;
 Matches 79; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNLMERVWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQLMHNGLKHLNLMERVWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SHEKSLGEANKADVNVLTAKSQ 115
 RESULT 3
 ID PTHY_CANPA STANDARD; PRT; 115 AA.
 AC P52212;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parathyroid;
 RX MEDLINE=95369696; PubMed=7642102;
 RA Rosol T.J., Steimeyer C.L., McCauley L.K., Greene A.,
 RA DeWille J.W., Capen C.C.;
 RT "Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone."
 RL Gene 160:241-243(1995).
 CC - FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC - SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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 CC -----
 DR EMBL: U15662; AAA82584.1;
 DR FIR: JC4202; JC4202.
 DR HSSP: P01268; L2WC.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR Pfam: P01279; Pthyrhorm_sub.
 DR ProDom: PD010687; Pthyrhorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; FC3BF77F1C8CFE56 CRC64;
 Query Match 86.7%; Score 366; DB 1; Length 115;
 Best Local Similarity 86.7%; Pred. No. 3.5e-33;
 Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNLMERVWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQLMHNGLKHLNLMERVWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SYOKSLGEADKADVDVLTAKSQ 115
 RESULT 4
 ID PTHY_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80056617; PubMed=388425;
 RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
 RA Potts J.T. Jr., Rich A.;
 RT "Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone."
 RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82037785; PubMed=6170060;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Introduction by molecular cloning of artifactual inverted sequences at the 5' terminus of the sense strand of bovine parathyroid hormone cDNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83105964; PubMed=6185374;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA."
 RL Mol. Cell. Endocrinol. 28:411-424(1982).
 RN [4]

RP SEQUENCE FROM N.A.
RX MEDLINE-84362483; PubMed-6086460;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RL parathyroid hormone.";
RL Gene 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE-74142666; PubMed-4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine parathyroid
RL hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE-71076162; PubMed-5531031;
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115.
RX MEDLINE-71063634; PubMed-5275384;
RA Brewer H.B. Jr., Ronan R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65.
RX MEDLINE-71091588; PubMed-4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RA Defotis L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RT "Synthesis of a biologically active N-terminal tetra-
RL tyrosine parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE-20090619; PubMed-10623601;
RA Marx U.C., Ademann K., Bayer F., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RL bPTH(1-37)."
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; V00106; CAA23439.1;
DR EMBL; J00024; AAA30747.1;
DR EMBL; K01938; AAA30749.1;
DR EMBL; M25082; AAA30748.1;
DR FIR; A24949; PTBO.
DR PDB; 1ZWC; 12-MAR-97.
DR InterPro; IPR001415; Parathyroid_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
FT HELIX 37 40

FT TURN 41 42
FT TURN 51 52
FT HELIX 53 60
FT TURN 61 63
SQ SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;
Query Match 85.1%; Score 359; DB 1; Length 115;
Best Local Similarity 85.5%; Pred. No. 2e-32;
Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 VSEIQLMNLGKHLNLSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQPRPKKEDNVLVE 60
DB 33 VSEIQFMNLGKHLNLSMERVEWLRKKLQDVHNFVALGASIAIYRDGSSQPRPKKEDNVLVE 92
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
DB 93 SHOKSLGEANKADVNVLTAKSQ 115
RESULT 5
PTHY_PIG STANDARD; PRT; 115 AA.
ID PTHY_PIG
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87316938; PubMed-3628009;
RA Schmelzer H.-J., Gross G., Wildera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RL preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE-76018954; PubMed-1164500;
RA Chu L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine parathyroid hormone. Identification, biosynthesis, and
RL partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE-74253317; PubMed-4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; X05722; CAA29193.1;
DR PIR; B26806; PTPG.
DR HSSP; P01270; 1BW.
DR InterPro; IPR001415; Parathyroid_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR SMART; SM00087; PTH; 1.

[illegible]


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CC CC Name=I;
CC CC ISOId=P29374-1; Sequence=Displayed;
CC CC Name=II;
CC CC ISOId=P29374-2; Sequence=VSP_004373;
CC CC Name=III;
CC CC ISOId=P29374-3; Sequence=VSP_004371, VSP_004372;
CC CC -----
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CC CC -----
CC CC EMBL; S66427; AAB28543.1; -
CC CC EMBL; S57133; AAB25833.1; -
CC CC EMBL; S57160; AAB25834.1; -
CC CC EMBL; S57162; AAB25835.2; -
CC CC PIR; I58383; I58383.
CC CC Genew; HGNC:9885; RBBP1.
CC CC NIM; 180201; -
CC CC GO; GO:0003634; C:nucleus; TAS.
CC CC GO; GO:0003515; F:protein binding activity; TAS.
CC CC GO; GO:0003700; F:transcription factor activity; TAS.
CC CC GO; GO:0003666; P:transcription from Pol II promoter; TAS.
CC CC InterPro; IPR001606; ARID.
CC CC InterPro; IPR000953; Chromo.
CC CC InterPro; IPR002999; Tudor.
CC CC Pfam; PF01388; ARID; 1.
CC CC SMART; SM00501; BRIGHT; 1.
CC CC SMART; SM00298; CHROMO; 1.
CC CC SMART; SM00333; TUDOR; 1.
CC CC Trans-acting factor; Nuclear protein; Alternative splicing.
CC CC TRANS-acting factor; RETINOBLASTOMA PROTEIN-BINDING
CC CC DOMAIN 951 964
CC CC FT VARSPLIC 1106 1174
CC CC FT VARSPLIC 1175 1175
CC CC FT VARSPLIC 1121 1174
CC CC FT CONFLICT 385 385
CC CC FT CONFLICT 618 618
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CC CC FT CONFLICT 779 779
CC CC FT CONFLICT 1178 1178
CC CC FT CONFLICT 1196 1201
CC CC FT CONFLICT 1257 1257
CC CC FT SEQUENCE 1257 AA; 142666 MW; F5C0AB6D6ED431DC CRC64;
CC CC Query Match 17.1%; Score 72; DB 1; Length 1257;
CC CC Best Local Similarity 26.8%; Pred. No. 6.8;
CC CC Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;
CC CC -----
CC CC 13 HLNSMERYEWLKKLQDVHN-FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANK 71
CC CC DDb 1179 NNNSTERSIFLQEKIQEIKYKMYSLKSEVATIDRRKRLKKKRDREV---SHAGASMSAS 1235
CC CC QY 72 ADVNVLTRAKS 82
CC CC DDb 1236 SDTGMSPSSSS 1246
CC CC -----
CC CC RESULT 10
CC CC UL25_HSV62
CC CC ID UL25_HSV62 STANDARD; PRT; 555 AA.
CC CC AC P52537;
CC CC DT 01-OCT-1996 (Rel. 34; Created)
CC CC DT 01-OCT-1996 (Rel. 34; Last sequence update)
CC CC DT 16-OCT-2001 (Rel. 40; Last annotation update)
CC CC DE Virus protein U50.
CC CC GN U50 OR KALLR.
CC CC OS Human herpesvirus (type 6 / strain 229) (HHV6).
CC CC -----
CC CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC CC Betaherpesvirinae; Roseolovirus.
CC CC NCBI_TaxID=36351;
CC CC [1]
CC CC SEQUENCE FROM N.A.
CC CC MEDLINE=95074921; PubMed=7983761;
CC CC RA Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
CC CC "Intragenomic linear amplification of human herpesvirus 6B orilyt
CC CC suggests acquisition of orilyt by transposition.";
CC CC RL J. Virol. 69:599-596(1995).
CC CC CC -|- FUNCTION: VIRION PROTEIN.
CC CC CC -|- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC CC EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AF157706; AAB06348.1; -
CC CC PIR; T44010; T44010.
CC CC InterPro; IPR002493; UL25.
CC CC Pfam; PF01499; UL25; 1.
CC CC SQ SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;
CC CC Query Match 16.5%; Score 69.5; DB 1; Length 555;
CC CC Best Local Similarity 35.4%; Pred. No. 5;
CC CC Matches 23; Conservative 10; Mismatches 27; Indels 5; Gaps 2;
CC CC -----
CC CC 23 LRKKLQDVHN-FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEA----NKADYVNLV 78
CC CC DDb 42 LRKKLQDVHN-FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEA----NKADYVNLV 78
CC CC QY 79 KAKSQ 83
CC CC DDb 101 KADTQ 105
CC CC -----
CC CC RESULT 11
CC CC GLMS_FUSNN STANDARD; PRT; 606 AA.
CC CC ID GLMS_FUSNN STANDARD; PRT; 606 AA.
CC CC AC Q8RG65;
CC CC DT 28-FEB-2003 (Rel. 41; Created)
CC CC DT 28-FEB-2003 (Rel. 41; Last sequence update)
CC CC DT 28-FEB-2003 (Rel. 41; Last annotation update)
CC CC DE Glucosamine-6-phosphate-6-phosphate aminotransferase [isomerizing]
CC CC (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
CC CC phosphate amidotransferase) (GPA) (L-glutamine-D-fructose-6-phosphate
CC CC amidotransferase) (Glucosamine-6-phosphate synthase).
CC CC GN GLMS OR FN0452.
CC CC OS Fusobacterium nucleatum (subsp. nucleatum).
CC CC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
CC CC Fusobacterium.
CC CC NCBI_TaxID=76856;
CC CC [1]
CC CC SEQUENCE FROM N.A.
CC CC STRAIN=ATCC 25586;
CC CC MEDLINE=21886394; PubMed=11889109;
CC CC RA Kapatral V., Anderson I., Ivanova N., Resnik G., Los T., Lykidis A.,
CC CC Bhatnagar V., Bhatnagar A., Bhatnagar A., Gardner W., Grechkin G., Zhu L.,
CC CC Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
CC CC Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
CC CC Fonstein M., Kyrpides N., Overbeek R.;
CC CC "Genome sequence and analysis of the oral bacterium Fusobacterium
CC CC nucleatum strain ATCC 25586.";
CC CC RL J. Bacteriol. 184:2005-2018(2002).
CC CC CC -|- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC CC converting fructose-6P into glucosamine-6P using glutamine as a
CC CC nitrogen source (By similarity).
CC CC -|- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate - L-
```

glutamate + D-glucosamine 6-phosphate.
 -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
 -1- SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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 EMBL; AE010557; AAL94648.1;
 HAMAP; MF_00164; -. 1.
 InterPro; IPR000583; GATase_2.
 InterPro; IPR005855; GLMS.
 InterPro; IPR001347; SIS.
 Pfam; PF00310; GATase_2; 1.
 Pfam; PF01380; SIS; 2.
 TIGRfams; TIGR01135; glms; 1.
 PROSITE; PS00443; GATASE_TYPE_II; 1.
 Transferase; Amidotransferase; Glutamine amidotransferase;
 Complete proteome.
 INIT_MET 0 0 BY SIMILARITY.
 DOMAIN 1 240 GLUTAMINE AMIDOTRANSFERASE.
 ACT_SITE 1 1 GATASE (BY SIMILARITY).
 ACT_SITE 601 601 ISOMERIZATION FRU-6P (BY SIMILARITY).
 SEQUENCE 506 AA; 67768 MW; D6AE271D47D5EA CRC64;
 Query Match 16.1%; Score 68; DB 1; Length 606;
 Best Local Similarity 25.6%; Pred. No. 8.1;
 Matches 21; Conservative 21; Mismatches 34; Indels 6; Gaps 3;
 QY 1 VSEIQLM-HNLGHLSMSEVWLRKQLQDVHNFVALGAPLADPRDAGSORPRKKENLV 59
 DB 433 ISDLSLKNVVLSEKEKIHDIKKIKNGFYLGRIDEKVARREGSKMKMEINYI- 491
 QY 60 ESHEKSL--GEANKADVNLTK 79
 DB 492 --HTEALPAGELKHGSLALIEK 511
 RESULT 12
 ID HSLU_VIBCH STANDARD; PRT; 443 AA.
 AC Q9KN07;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ATP-dependent hsl protease ATP-binding subunit hslu.
 GN HSLU OR VC2674.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=El Tor N16961 / Serotype O1;
 RC MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bess S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RL Nature 406:477-483(2000).
 CC -1- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
 CC COMPLEX (BY SIMILARITY).

-1- SUBUNIT: Interacts with hslv (By similarity).
 -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 -1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
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 EMBL; AE004333; AAF95815.1;
 DR EMBL; E82046; E82046.
 DR HSP; P32168; IDO2.
 DR TIGR; VC2674; -. 1.
 HAMAP; MF_00249; -. 1.
 InterPro; IPR003593; AAA_ATPase.
 InterPro; IPR003595; AAA_ATPase_Centr.
 InterPro; IPR004491; Hsp_Hslvu.
 Pfam; PF00004; AAA; 1.
 SMART; SM00382; AAA; 1.
 TIGRfams; TIGR00390; hslu; 1.
 KW Chaperone; ATP-binding; Complete proteome.
 FT NF_BIND 57 64 ATP (POTENTIAL).
 SQ SEQUENCE 443 AA; 49900 MW; DAEL3E82FAB6A38F CRC64;
 Query Match 15.9%; Score 67; DB 1; Length 443;
 Best Local Similarity 28.8%; Pred. No. 7.3;
 Matches 19; Conservative 16; Mismatches 27; Indels 4; Gaps 2;
 QY 13 HLSMERVEWLRKQLQDVHNFVALGAPLADPRDAGSORPRKKEDNVLSHEKSL--GEAN 70
 DB 112 HQAMEKVKFRAELAEAEVRLDALLPP--PDANGAQEKEENSSTQVFRKKLRGQLN 169
 QY 71 KADVNV 76
 DB 170 DKEIEI 175
 RESULT 13
 ID UL25_HSV6G STANDARD; PRT; 378 AA.
 AC P52536;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Virion protein U50 (Fragment).
 GN U50 OR LF3.
 OS Human herpesvirus (type 6 / strain GS) (HHV6).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseolovirus.
 OX NCBI_TaxID=10369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91374623; PubMed=1654455;
 RA Josephs S.F., Ablashi D.V., Salahuddin S.Z., Jagodzinski L.L.,
 RA Wong-Staal F., Gallo R.C.;
 RT "Identification of the human herpesvirus 6 glycoprotein H and
 putative large tegument protein genes.";
 RL J. Virol. 65:5597-5604(1991).
 CC -1- FUNCTION: VIRION PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
 CC EBV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
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```
DR EMBL; S57509; AAB19777.1; -.
DR PIR; F56653; F56653.
DR InterPro: IPR002493; UL25.
DR Pfam; PF01499; UL25.1.
FT NONTER 378 378
SQ SEQUENCE 378 AA; 43459 MW; BEBB2EF416270AB6 CRC64;

Query Match
Best Local Similarity 15.8%; Score 66.5; DB 1; Length 378;
Matches 22; Conservative 11; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKKLQDVHNFVALGAPLAPRDSQRPRKKEDNVLVSHESKSLGEA-----NKADVNYLT 78
DB 42 LREKIDQGHDRKLLRMRLKLTDLALQKKMQKSDVL-NSHLKAIEDALLFTNDGEVNYET 100

QY 79 KAKSQ 83
DB 101 KADAQ 105

RESULT 14
UL25_RSV6U STANDARD; PRT; 555 AA.
AC PS2387;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Viron protein US0.
GN US0 OR BHRF3.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HRV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OC NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266321; PubMed=7747482;
RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA Martin M.E., Efsthaliou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution.";
RL Virology 209:29-51(1995).
[2]
RP SEQUENCE OF 1-378 FROM N.A.
RX MEDLINE=93091236; PubMed=1333836;
RA Gompels U.A., Carrs A.L., Sun N., Arrand J.R.;
RA "Infectivity determinants encoded in a conserved gene block of human
RT herpesvirus-6.";
RL DNA Seq. 3:25-39(1992).
CC -!- FUNCTION: VIRION PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC EH-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83413; CAA58384.1; -.
DR EMBL; X64320; CAA45605.1; -.
DR InterPro: IPR002493; UL25.
DR Pfam; PF01499; UL25; 1.
SQ SEQUENCE 555 AA; 63594 MW; BA0C879FF56130D4 CRC64;

Query Match
Best Local Similarity 15.8%; Score 66.5; DB 1; Length 555;
Matches 22; Conservative 11; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKKLQDVHNFVALGAPLAPRDSQRPRKKEDNVLVSHESKSLGEA-----NKADVNYLT 78
DB 42 LREKIDQGHDRKLLRMRLKLTDLALQKKMQKSDVL-NSHLKAIEDALLFTNDGEVNYET 100
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QY 79 KAKSQ 83
DB 101 KADAQ 105
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RESULT 15

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DPO4_CLOAB
ID DPO4_CLOAB STANDARD; PRT; 396 AA.
AC Q97MB3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase IV (EC 2.7.7.7) (Pol IV).
GN DINB OR CAC0285.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Poorly processive, error-prone DNA polymerase involved
CC in untargeted mutagenesis. Copies undamaged DNA at stalled
CC replication forks, which arise in vivo from mismatched or
CC misaligned primer ends. These misaligned primers can be extended
CC by polIV. Exhibits no 3'-5' exonuclease (proofreading) activity.
CC May be involved in translesional synthesis, in conjunction with
CC the beta clamp from polIII (By similarity).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + (DNA)(N).
CC -!- COFACTOR: Binds two magnesium ions (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
CC -!- SIMILARITY: Contains 1 unuc domain.
CC -----
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CC -----
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DR EMBL; AE007542; AAK78266.1; -.
DR PIR; G96934; G96934.
DR HAMAP; MF_01113; -.
DR InterPro: IPR001126; UMUC_like.
DR Pfam; PF00817; IMS; 1.
DR PROSITE; PS50173; UMUC; 1.
KW Transferrase; DNA-directed DNA polymerase; DNA replication; DNA repair;
KW DNA-binding; Mutator protein; Magnesium; Complete proteome.
FT SITE 5 192 UMUC.
FT SITE 14 14
FT ACT_SITE 112 112 SUBSTRATE DISCRIMINATION (BY SIMILARITY).
FT METAL 9 9 BY SIMILARITY.
FT METAL 111 111 MAGNESIUM (BY SIMILARITY).
FT METAL 111 111 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 396 AA; 45363 MW; A19826BCBC0D5410 CRC64;
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Query Match
Best Local Similarity 15.6%; Score 66; DB 1; Length 396;
Matches 26; Conservative 11; Mismatches 33; Indels 14; Gaps 4;
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```
QY 1 VSEIQLMHNGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRD---AGSORPKKEDNY 57
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Search completed: October 9, 2003, 08:11:21
Job time : 18.1045 secs


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OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Devey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382952; AAK63071.1;
DR InterPro; IPR001415; Parathyrd_hrm.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrdhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match
Best Local Similarity 19.9%; Score 84; DB 11; Length 31;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLKHLNSME 18
DB 14 VSEIQLMHNGLKHLASME 31

RESULT 6
Q918E9 PRELIMINARY; PRT; 163 AA.
AC Q918E9
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Parathyroid hormone-related protein precursor.
GN PTHRP.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
ELgar G., Clark M.S.;
RT "Genomic structure and expression of parathyroid hormone-related
protein in a teleost, Fugu rubripes."
RL Gene 250:67-79(2000).
DR EMBL; AJ249391; CAB94712.1;
DR HSP; P12272; 1BZG.
DR InterPro; IPR001415; Parathyrd_hrm.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD013225; PTH_related; 1.
KW SIGNAL.
FT SIGNAL 1
FT SIGNAL 34
SQ SEQUENCE 163 AA; 18698 MW; 3AC5F2C764732278 CRC64;

Query Match
Best Local Similarity 18.8%; Score 79.5; DB 13; Length 163;
Matches 30; Conservative 10; Mismatches 35; Indels 35; Gaps 4;

QY 1 VSEIQLMHNGLKHLNSMERVLRKLDQVHNFVALGAPLAPRDAGSQRPKRKEDNVLVE 60
DB 39 VSHAQLMHDKRSLOEFRRLWHLKLEEVH-----ANEAPPVOSRTOTQTSFGN 90
QY 61 S-HKSLG-----EANKA-----DYNVLTAKSQ 83
DB 91 SLHEKPPGATKNLPDRFSLDREGTNLPQETNKALAYKDQPLKATRKKK 140

RESULT 7
Q918U2 PRELIMINARY; PRT; 162 AA.
ID Q918U2

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AC Q918U2; 2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Parathyroid hormone-related protein.
GN PTHRP.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RX MEDLINE=20304721; PubMed=10843788;
RA Flanagan J.A., Power D.M., Bendell L.A., Guerreiro P.M., Fuentes J.,
Clark M.S., Canario A.V., Danks J.A., Brown B.L., Ingleton P.M.;
RT "Cloning of the cDNA for sea bream (Sparus aurata) parathyroid
hormone-related protein."
RL Gen. Comp. Endocrinol. 118:373-382(2000).
DR EMBL; AF197904; AAF79073.1;
DR HSP; P12272; 1BZG.
DR InterPro; IPR001415; Parathyrd_hrm.
DR ProDom; PD013225; PTH_related; 1.
DR ProDom; PD013225; PTH_related; 1.
SQ SEQUENCE 162 AA; 18722 MW; 5EBD5E07F9E5EDC9 CRC64;

Query Match
Best Local Similarity 18.6%; Score 78.5; DB 13; Length 162;
Matches 31; Conservative 11; Mismatches 32; Indels 35; Gaps 5;

QY 1 VSEIQLMHNGLKHLNSMERVLRKLDQVHNFVALGAPLAPRDAGSQRPKRKEDNVLVE 50
DB 39 VSHAQLMHDKRSLOEFRRLWHLKLEEVH-----TADDRPVQGR-----TQSOTFSGNAL-- 90
QY 61 SHEKSLG-----EANKA-----DYNVLTAKSQ 83
DB 91 HEKPPGATKNLPDRFSLDREGTNLPQETNKALAYKDQPLKATRKKK 138

RESULT 8
Q99WC5 PRELIMINARY; PRT; 565 AA.
ID Q99WC5
AC Q99WC5
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE DNA polymerase III gamma and tau subunits.
GN DNAX OR SAV0478 OR SA0436.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878; 158879;
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11416146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mikitani Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sakimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003359; BAB56640.1;
DR EMBL; AP003130; BAB41666.1;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003593; AAA_ATPase_cent.

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DR InterPro: IPR001270; Chaprinin_clpA/B.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000862; RFCdomain.
DR Pfam: PF00004; AAA; 1.
DR PRINTS: PR00300; CLPPROTEASEA.
DR SMART: SMO0382; AAA; 1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00214; FBP; 1.
KW Complete proteome.
SQ SEQUENCE 565 AA; 63471 MW; F29A7F07095F02AA CRC64;

Query Match      17.3%; Score 73; DB 16; Length 565;
Best Local Similarity 29.4%; Pred. No. 12;
Matches 20; Conservative 15; Mismatches 23; Indels 10; Gaps 2

QY 14 LNSMERVEWLRRKKLDVHNEVALGAPLAPRDAGSQRP-----RKEDNVLVESHEKSLGEA 69
DB 376 LQRNQGLE-----QLTKLAQGVSAPAQKSKPKRGIOKSNAFSMQIATKVLDKA 429
|||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 70 NKADVNLV 77
DB 430 NKADIKLL 437
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

RESULT 9
QB8YA2          PRELIMINARY; PRT; 140 AA.
ID QB8YA2;
AC QB8YA2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Retinoblastoma-binding protein 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA THE RIKEN Genome Exploration Research Group Phase I & II Team;
RT *Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.*;
RL Nature 420:563-573(2002).
DR ENBL: AK041444; BAC30948.1; -.
FT NON_TER 1
SQ SEQUENCE 140 AA; 15988 MW; 15CE80236A5E9930 CRC64;

Query Match      17.1%; Score 72; DB 11; Length 140;
Best Local Similarity 26.8%; Pred. No. 3;
Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2

QY 13 HNSMERVEWLRRKKLDVHN- FVALGPALAPRDAGSQRPKRKEDNVLVESHEKSLGEANK 71
DB 62 NMNSTERISFLQELQEIIRKYMSLKSEVATIDRRRKLKKKDREV---SHAGASMSAS 118
::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
::|NMNSTERISFLQELQEIIRKYMSLKSEVATIDRRRKLKKKDREV---SHAGASMSAS 118

QY 72 ADVNYLTRAKS 82
DB 119 SDTGMSPSSSS 129.
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||

RESULT 10
QB8Y08          PRELIMINARY; PRT; 565 AA.
ID QB8Y08;
AC QB8Y08;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE DNA polymerase III gamma and tau subunits.
GN DNAX OR W0433.
OS Staphylococcus aureus (strain MW2).

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RESULT 14
Q8LMT1

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QY      58      -----LVESHEKSLGEANKADNVNLTAKSQ 83
DB      175     NDADTPDGPDTIVTKKKGKSHKQKIKSPFAGQSTRPDVTIAAPAKSE 226

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Search completed: October 9, 2003, 08:13:31
Job time : 77.3284 secs

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RESULT 15
Q8LHC6 PRELIMINARY; PRT; 362 AA.
AC Q8LHC6
AC Q8LHC6:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 23, Last annotation update)
DE P0458E05.24 protein.
DE P0458E05.24
DE P0458E05.24
GN Oryza sativa (japonica cultivar-group).
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID:39947;
OX {}
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0458E05."
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004365; BAC05624.1;
DR Gramene; Q8LHC6;
DR SEQUENCE 362 AA; 39366 MW; B87DEB28851E6740 CRC64;

Query Match 16.0%; Score 67.5; DB 10; Length 362;
Best Local Similarity 20.5%; Pred. No. 29;
Matches 23; Conservative 21; Mismatches 37; Indels 31; Gaps 3;

QY 1 VSEIQLMHNIGKHLNSMERVWELRKKLQD-VHNFVALGAPLAPDAGSQRPKKEDNV-- 57
DB 117 LSEHLRYRNLNQLNGPFAEKDGLAKYVKLVNPIRIFNS--KPMKASKSKNSRENLPI 174

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:57 ; Search time 21.0597 Seconds
(without alignments)
166.755 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHNLGKHLNSMERY.....KSLGEANKADVNLTAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_5/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_5/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_5/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_5/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_5/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_5/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	98.8	83	4 US-10-002-818-2	Sequence 2, Appli
2	417	98.8	84	1 US-07-863-014-2	Sequence 2, Appli
3	417	98.8	84	1 US-08-332-453-2	Sequence 2, Appli
4	417	98.8	84	1 US-08-689-190-2	Sequence 2, Appli
5	417	98.8	84	2 US-08-835-231-9	Sequence 9, Appli
6	417	98.8	84	2 US-08-805-918-3	Sequence 3, Appli
7	417	98.8	84	3 US-09-108-661-9	Sequence 9, Appli
8	417	98.8	84	4 US-10-002-818-1	Sequence 1, Appli
9	417	98.8	84	5 PCT-US95-15800-25	Sequence 25, Appli
10	412	97.6	84	2 US-08-142-551B-1	Sequence 1, Appli
11	412	97.6	84	2 US-08-411-726-1	Sequence 1, Appli
12	407	96.4	84	1 US-07-707-114-1	Sequence 1, Appli
13	368	87.2	84	1 US-07-773-098-2	Sequence 2, Appli
14	364	86.3	84	2 US-08-733-446-5	Sequence 5, Appli
15	359	85.1	84	1 US-07-773-098-1	Sequence 1, Appli
16	356	84.4	81	2 US-08-733-446-4	Sequence 4, Appli
17	352	83.4	84	1 US-07-776-272-14	Sequence 14, Appli
18	351	83.2	80	2 US-08-733-446-3	Sequence 3, Appli
19	350	82.9	84	1 US-07-773-098-9	Sequence 9, Appli
20	350	82.9	84	1 US-07-773-098-10	Sequence 10, Appli
21	347	82.2	79	2 US-08-733-446-2	Sequence 2, Appli
22	342	81.0	78	2 US-08-733-446-1	Sequence 1, Appli
23	341	80.8	84	1 US-07-773-098-7	Sequence 7, Appli
24	341	80.8	84	1 US-07-773-098-8	Sequence 8, Appli
25	337	79.9	84	3 US-09-044-536A-36	Sequence 36, Appli
26	248	58.8	51	3 US-09-044-536A-7	Sequence 7, Appli
27	248	58.8	51	4 US-10-002-818-3	Sequence 3, Appli

28	237	56.2	50	2	US-08-142-551B-119	Sequence 119, Appli
29	193	45.7	38	1	US-08-112-024-1	Sequence 1, Appli
30	193	45.7	38	1	US-08-232-849-1	Sequence 1, Appli
31	193	45.7	38	2	US-08-625-586-1	Sequence 1, Appli
32	193	45.7	38	3	US-09-128-401-1	Sequence 1, Appli
33	187	44.3	37	1	US-08-440-117-1	Sequence 1, Appli
34	187	44.3	37	3	US-09-088-738A-16	Sequence 16, Appli
35	186	44.1	38	5	PCT-US95-15800-29	Sequence 29, Appli
36	183	43.4	36	1	US-08-256-363-4	Sequence 4, Appli
37	179	42.4	34	1	US-08-256-363-2	Sequence 2, Appli
38	179	42.4	35	1	US-08-256-363-3	Sequence 3, Appli
39	179	42.4	36	1	US-08-112-024-2	Sequence 2, Appli
40	175	41.5	33	1	US-08-256-363-1	Sequence 1, Appli
41	175	41.5	34	1	US-07-765-373-1	Sequence 1, Appli
42	175	41.5	34	1	US-08-033-099-1	Sequence 1, Appli
43	175	41.5	34	1	US-08-262-495C-1	Sequence 1, Appli
44	175	41.5	34	1	US-07-915-247A-1	Sequence 1, Appli
45	175	41.5	34	1	US-08-443-863-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-002-818-2
; Sequence 2, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroidism
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002.818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 2
; LENGTH: 83
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-2

Query Match	98.8%;	Score 417;	DB 4;	Length 83;
Best Local Similarity	98.8%;	Pred. No. 1.8e-44;		
Matches	82;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;
Oy	1	VSEIQLMHNLGKHLNSMERYEWLRRKLDQVHNFVALGAPLAPRDAGSORPKKEDNVLVE	60	
Db	1	VSEIQLMHNLGKHLNSMERYEWLRRKLDQVHNFVALGAPLAPRDAGSORPKKEDNVLVE	60	
Oy	61	SHEKSLGEANKADVNLTAKSQ	83	
Db	61	SHEKSLGEANKADVNLTAKSQ	83	

RESULT 2
US-07-863-014-2
; Sequence 2, Application US/07863014
; Patent No. 5382658
; GENERAL INFORMATION:
; APPLICANT: KRONIS, K. Anne
; APPLICANT: BOZZATO, Richard P.
; TITLE OF INVENTION: STABILITY-ENHANCED VARIANTS OF PARATHYROID HORMONE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,014
FILING DATE: 19920403
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/163 ALLE
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-863-014-2

Query Match 98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIOLMNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
Db 2 VSEIOLMNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 3
US-08-332-453-2
Sequence 2, Application US/08332453
Patent No. 559792
GENERAL INFORMATION:
APPLICANT: KRONIS, K. Anne
APPLICANT: BOZZATO, Richard P.
TITLE OF INVENTION: BONE-STIMULATING, NON-VASOACTIVE
TITLE OF INVENTION: PARATHYROID HORMONE VARIANTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,453
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,680
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/182 ALLE
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109

TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-453-2

Query Match 98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIOLMNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
Db 2 VSEIOLMNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 4
US-08-689-190-2
Sequence 2, Application US/08689190
Patent No. 5714349
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, Takao
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D.
REGISTRATION NUMBER: 30,901
REFERENCE/DOCKET NUMBER: 41,288
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-689-190-2

Query Match 98.8%; Score 417; DB 1; Length 84;

Best Local Similarity 98.8%; Pred. No. 1.8e-44; Mismatches 0; Indels 0; Gaps 0;
Matches 82; Conservative 1;

QY 1 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 60
|||||
Db 2 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 61
|||||
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||
Db 62 SHEKSLGEADKADVNLTKAKSQ 84
|||||

RESULT 5

US-08-835-231-9
; Sequence 9, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284uyuk1
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,231
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271439
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41614-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-835-231-9

Query Match 98.8%; Score 417; DB 2; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

US-08-805-918-3
; Sequence 3, Application US/08805918
; Patent No. 5885821
; GENERAL INFORMATION:

; APPLICANT: MAGOTA, Koji
; APPLICANT: MASUDA, Toyofumi
; APPLICANT: SUZUKI, Yuji
; APPLICANT: YABUTA, Masayuki
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF SECRETORY KEX2
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,918
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-073217
FILING DATE: 04-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-352580
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-805-918-3

Query Match 98.8%; Score 417; DB 2; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 60
|||||
Db 2 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 61
|||||
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||
Db 62 SHEKSLGEADKADVNLTKAKSQ 84
|||||

RESULT 7

US-09-108-661-9
; Sequence 9, Application US/09108661
; Patent No. 6287806
; GENERAL INFORMATION:
; APPLICANT: KUSHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-9

Query Match 98.8%; Score 417; DB 3; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
DB 2 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 61
QY 61 SHEKSLGEAKADVNVLTAKSQ 83
DB 62 SHEKSLGEAKADVNVLTAKSQ 84

RESULT 8

US-10-002-818-1

; Sequence 1, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathy
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002,818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-1
Query Match 98.8%; Score 417; DB 4; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
DB 2 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 61
QY 61 SHEKSLGEAKADVNVLTAKSQ 83
DB 62 SHEKSLGEAKADVNVLTAKSQ 84
RESULT 9
PCT-US95-15800-25
; Sequence 25, Application PC/TUS9515800
; GENERAL INFORMATION:
; APPLICANT: Bionbraska, Inc.
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING
; TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRUCTS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 Norwest Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15800
; FILING DATE: 07-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,530
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.45USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
PCT-US95-15900-25

Query Match 98.8%; Score 417; DB 5; Length 84;

Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNKGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60
DB 2 VSEIQLMHNKGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61
QY 61 SHEKSLGEADKADVNVLTKAKSQ 83
DB 62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 10

US-08-142-551B-1

; Sequence 1, Application US/08142551B

; Patent No. 5814603

; GENERAL INFORMATION:

; APPLICANT: Oldenburg, Kevin R.

; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND

; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME

; NUMBER OF SEQUENCES: 132

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: US

; ZIP: 22313

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/142.551B

; FILING DATE: 25-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/077,296

; FILING DATE: 14-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/898,219

; FILING DATE: 12-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/965,677

; FILING DATE: 22-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.

; REGISTRATION NUMBER: 30,113

; REFERENCE/DOCKET NUMBER: 000324-010

; TELEPHONE: (415) 854-7400

; TELEFAX: (415) 854-8275

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 84 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..84

; OTHER INFORMATION: /note= "84 amino acid PTH"

US-08-142-551B-1

Query Match

97.6%; Score 412; DB 2; Length 84;

Best Local Similarity 97.6%; Pred. No. 7.5e-44;
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNKGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60
DB 2 VSEIQLMHNKGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61
QY 61 SHEKSLGEADKADVNVLTKAKSQ 83
DB 62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 11

US-08-411-726-1

; Sequence 1, Application US/08411726

; Patent No. 5880093

; GENERAL INFORMATION:

; APPLICANT: Bagnoli, Franco

; TITLE OF INVENTION: Use of Parathormone, Its Biologically

; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for the Prepar

; TITLE OF INVENTION: Pharmaceutical Compositions Useful for the Treatment of

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenyon & Kenyon

; STREET: 1 Broadway

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

; SOFTWARE: Wordperfect 6.1 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411.726

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/02755

; FILING DATE: 08-OCT-1993

; APPLICATION NUMBER: MI-92A002331

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: PALMESE, Maria Luisa

; REGISTRATION NUMBER: 34,402

; REFERENCE/DOCKET NUMBER: 2111/1300

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-425-7200

; TELEFAX: 212-425-5288

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 84 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-411-726-1

Query Match

97.6%; Score 412; DB 2; Length 84;

Best Local Similarity 97.6%; Pred. No. 7.5e-44;
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNKGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 60
DB 2 VSEIQLMHNKGLKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLYE 61
QY 61 SHEKSLGEADKADVNVLTKAKSQ 83
DB 62 SHEKSLGEADKADVNVLTKAKSQ 84

RESULT 12

US-07-707-114-1
; Sequence 1, Application US/07707114
; Patent No. 5208041
; GENERAL INFORMATION:
; APPLICANT: SINDREY, Dennis R.
; TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID
; HORMONE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/707.114
; FILING DATE: 19910523
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/147 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; IMMEDIATE SOURCE:
; CLONE: hPTH
US-07-707-114-1

Query Match 96.4%; Score 407; DB 1; Length 84;
Best Local Similarity 96.4%; Pred. No. 3.1e-43;
Matches 80; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRAGSORPRKKEDNVLYE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRAGSORPRKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEANKADVNLTKAKSQ 84

RESULT 13
US-07-773-098-2
; Sequence 2, Application US/0773098
; Patent No. 5317010
; GENERAL INFORMATION:
; APPLICANT: PANG, Peter K.T.
; APPLICANT: JIE, Shan
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS
; TITLE OF INVENTION: OSTEOOPOROTIC CONTROL AGENTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Nikaido, Marmelstein, Kubovcik &
; ADDRESSEE: Murray
; STREET: 1725 K Street, N.W., Suite 1000
; CITY: Washington D.C.
; COUNTRY: United States of America

ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/773.098
; FILING DATE: 19911010
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,890
; REFERENCE/DOCKET NUMBER: 901930
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-773-098-2

Query Match 87.2%; Score 368; DB 1; Length 84;
Best Local Similarity 88.0%; Pred. No. 2.1e-38;
Matches 73; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRAGSORPRKKEDNVLYE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGASIAVRDGSORPRKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHKSLGEADKADVNLTKAKPQ 84

RESULT 14
US-08-733-446-5
; Sequence 5, Application US/08733446
; Patent No. 5856138
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTAINS AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733.446
; FILING DATE: 18-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/402.970
; FILING DATE:
; APPLICATION NUMBER: US/07/926.787
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964

REFERENCE/DOCKET NUMBER: 42025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Mutation
LOCATION: 8 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,
LOCATION: 18 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,
LOCATION: 34 Xaa-Cys or Phe, 35 Xaa-Cys or Val,
LOCATION: 37 Xaa-Cys or Leu, 39 Xaa-Cys or Ala,
LOCATION: 41 Xaa-Cys or Leu, 43 Xaa-Cys or Pro, 44 Xaa-Cys or Arg
IDENTIFICATION METHOD: E
US-08-733-446-5

Query Match 86.3%; Score 364; DB 2; Length 84;
Best Local Similarity 88.0%; Pred. No. 6.7e-38;
Matches 73; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEADKADVNLTKAKSQ 84

RESULT 15

US-07-773-098-1
Sequence 1, Application US/07773098
Patent No. 5317010
GENERAL INFORMATION:
APPLICANT: PANG, Peter K.T.
APPLICANT: JIE, Shan
TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS
TITLE OF INVENTION: OSTEOPOROTIC CONTROL AGENTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Nikolaïdo, Marmelstein, Kubovcik &
ADDRESSEE: Murray
STREET: 1725 K Street, N.W., Suite 1000
CITY: Washington D.C.
COUNTRY: United States of America
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/773,098
FILING DATE: 19911010
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,890
REFERENCE/DOCKET NUMBER: 901930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-773-098-1

Query Match 85.1%; Score 359; DB 1; Length 84;
Best Local Similarity 85.5%; Pred. No. 2.8e-37;
Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEADKADVNLTKAKSQ 84

Search completed: October 9, 2003, 08:15:10
Job time: 23.0597 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:10:52 ; Search time 154.851 Seconds
(without alignments)
86.365 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHNLCGKHLNSMERV.....KSLGEANKADYNVLTAKSQ 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_AA:*
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	422	100.0	83	10	US-09-928-047B-1
2	422	100.0	83	12	US-09-928-048A-4
3	422	100.0	84	10	US-09-928-047B-5
4	422	100.0	84	12	US-09-928-048A-3
5	422	100.0	84	15	US-10-215-770-1
6	418	99.1	82	10	US-09-928-047B-2
7	417	98.8	84	9	US-09-169-786-1
8	417	98.8	84	11	US-09-843-221A-10
9	417	98.8	84	11	US-09-898-398-1
10	417	98.8	115	15	US-10-157-031-50
11	400	94.8	78	10	US-09-928-047B-4
12	395	93.6	78	11	US-09-843-221A-12
13	366	86.7	84	15	US-10-215-770-3
14	359	85.1	84	9	US-09-879-257A-49
15	359	85.1	84	15	US-10-215-770-4

16	355	84.1	84	15	US-10-215-770-2	Sequence 2, Appli
17	315	74.6	84	11	US-09-843-221A-11	Sequence 11, Appli
18	311	73.7	84	15	US-10-215-770-5	Sequence 5, Appli
19	286	67.8	57	10	US-09-928-047B-8	Sequence 8, Appli
20	253	60.0	51	10	US-09-928-047B-3	Sequence 3, Appli
21	253	60.0	51	12	US-09-928-048A-5	Sequence 5, Appli
22	247	58.5	50	10	US-09-928-047B-7	Sequence 7, Appli
23	247	58.5	50	12	US-09-928-048A-7	Sequence 7, Appli
24	224	53.1	44	11	US-09-843-221A-13	Sequence 13, Appli
25	193	45.7	37	11	US-09-843-221A-15	Sequence 15, Appli
26	193	45.7	38	9	US-09-169-786-4	Sequence 4, Appli
27	193	45.7	38	11	US-09-843-221A-14	Sequence 14, Appli
28	193	45.7	38	12	US-10-245-707-1	Sequence 1, Appli
29	188	44.5	40	15	US-10-014-162-11	Sequence 11, App
30	187	44.3	37	12	US-10-168-185-9	Sequence 9, Appli
31	175	41.5	34	9	US-09-169-786-3	Sequence 3, Appli
32	175	41.5	34	10	US-09-928-047B-6	Sequence 6, Appli
33	175	41.5	34	11	US-09-843-221A-16	Sequence 16, Appli
34	175	41.5	34	11	US-09-843-221A-20	Sequence 20, Appli
35	175	41.5	34	11	US-09-843-221A-161	Sequence 161, App
36	175	41.5	34	12	US-09-928-048A-6	Sequence 6, Appli
37	175	41.5	34	12	US-10-361-928-1	Sequence 1, Appli
38	175	41.5	34	12	US-10-361-928-2	Sequence 2, Appli
39	175	41.5	34	12	US-10-361-928-5	Sequence 5, Appli
40	175	41.5	34	12	US-10-361-928-8	Sequence 8, Appli
41	175	41.5	34	12	US-10-340-484-15	Sequence 15, Appli
42	175	41.5	34	12	US-10-340-484-16	Sequence 16, Appli
43	175	41.5	34	14	US-10-016-403-5	Sequence 5, Appli
44	175	41.5	34	14	US-10-097-079-1	Sequence 1, Appli
45	175	41.5	42	12	US-10-325-021-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-1

Query Match 100.0%; Score 422; DB 10; Length 83;
Best Local Similarity 100.0%; Pred. No. 2,4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VSEIQLMHNLCGKHLNSMERVWLRRKKLQDVHNFALGAPLAPRDAGSORPKKEDNVLVE 60
Db 1 VSEIQLMHNLCGKHLNSMERVWLRRKKLQDVHNFALGAPLAPRDAGSORPKKEDNVLVE 60
Oy 61 SHEKSLGEANKADYNVLTAKSQ 83
Db 61 SHEKSLGEANKADYNVLTAKSQ 83
RESULT 2
US-09-928-048A-4
; Sequence 4, Application US/09928048A
; Publication No. US20030138658A1

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; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-4

Query Match      100.0%; Score 422; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
Db 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 61 SHEKSLGEANKADVNVLTAKSQ 83

RESULT 3
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-5

Query Match      100.0%; Score 422; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 4
US-09-928-048A-3
; Sequence 3, Application US/09928048A
; Publication No. US20030138658A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
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; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-3

Query Match      100.0%; Score 422; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 5
US-10-215-770-1
; Sequence 1, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-770-1

Query Match      100.0%; Score 422; DB 15; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 60
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 6
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
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SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 82

TYPE: PRT

ORGANISM: Homo sapiens

US-09-928-047B-2

Query Match 99.1%; Score 418; DB 10; Length 82;

Best Local Similarity 100.0%; Pred. No. 7.2e-43;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVES 61

Db 1 SEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVES 60

QY 62 HEKSLGEANKADVNVLTKAKSQ 83

Db 61 HEKSLGEANKADVNVLTKAKSQ 82

RESULT 7

US-09-169-786-1

Sequence 1, Application US/09169786B

Patent No. US20020025929A1

GENERAL INFORMATION:

APPLICANT: Sato, Masahiko

TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE

FILE REFERENCE: X-11480

CURRENT APPLICATION NUMBER: US/09/169,786B

EARLIER FILING DATE: 1998-10-09

EARLIER APPLICATION NUMBER: US 60/061,800

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 84

TYPE: PRT

ORGANISM: Homo sapiens

US-09-169-786-1

Query Match 98.8%; Score 417; DB 9; Length 84;

Best Local Similarity 98.8%; Pred. No. 9.8e-43;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVE 60

Db 2 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83

Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 8

US-09-843-221A-10

Sequence 10, Application US/09843221A

Publication No. US20030039554A1

GENERAL INFORMATION:

APPLICANT: KOSTENIUK, PAUL

APPLICANT: LIU, CHUAN-FA

TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H

FILE REFERENCE: A-665B

CURRENT APPLICATION NUMBER: US/09/843,221A

EARLIER FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: 60/266,673

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/214,860

PRIOR FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/200,053

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10

LENGTH: 84

TYPE: PRT

ORGANISM: Homo sapiens

US-09-843-221A-10

Query Match 98.8%; Score 417; DB 11; Length 84;

Best Local Similarity 98.8%; Pred. No. 9.8e-43;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVE 60

Db 2 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83

Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 9

US-09-898-398-1

Sequence 1, Application US/09898398

Publication No. US20030082179A1

GENERAL INFORMATION:

APPLICANT: Hutchison, James Scott

TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS

FILE REFERENCE: A1713

CURRENT APPLICATION NUMBER: US/09/898,398

CURRENT FILING DATE: 2001-07-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 84

TYPE: PRT

ORGANISM: Homo sapiens

US-09-898-398-1

Query Match 98.8%; Score 417; DB 11; Length 84;

Best Local Similarity 98.8%; Pred. No. 9.8e-43;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVE 60

Db 2 VSEIQLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQPRKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNVLTKAKSQ 83

Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 10

US-10-157-031-50

Sequence 50, Application US/10157031

Publication No. US20030108890A1

GENERAL INFORMATION:

APPLICANT: Baranova, A. V.

APPLICANT: Yankovsky, N. K.

APPLICANT: Kozlov, A. P.

APPLICANT: Lobashev, A. V.

APPLICANT: Kravchuk, L. L.

TITLE OF INVENTION: In silico screening for phenotype-associated sequ

FILE REFERENCE: 2760-103

CURRENT APPLICATION NUMBER: US/10/157,031

CURRENT FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 415

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-10-157-031-50

Query Match 98.8%; Score 417; DB 15; Length 115;
Best Local Similarity 98.8%; Pred. No. 1.4e-42;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
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DB 33 VSEIQMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 92
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QY 61 SHEKSGEANKADVNLTKAKSQ 83
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DB 93 SHEKSGEANKADVNLTKAKSQ 115
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RESULT 11
US-09-928-047B-4
; Sequence 4, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-4

Query Match 94.8%; Score 400; DB 10; Length 78;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 65
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DB 1 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 60
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QY 66 LGEANKADVNLTKAKSQ 83
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DB 61 LGEANKADVNLTKAKSQ 78
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RESULT 12
US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-12

Query Match 93.6%; Score 395; DB 11; Length 78;
Best Local Similarity 98.7%; Pred. No. 4e-40;
Matches 77; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 65
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DB 1 LMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 60
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QY 66 LGEANKADVNLTKAKSQ 83
|||||

DB 61 LGEANKADVNLTKAKSQ 78
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RESULT 13
US-10-215-770-3
; Sequence 3, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Dog
US-10-215-770-3

Query Match 86.7%; Score 366; DB 15; Length 84;
Best Local Similarity 86.7%; Pred. No. 1.4e-36;
Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSEIQMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
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DB 2 VSEIQMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 61
|||||

QY 61 SHEKSGEANKADVNLTKAKSQ 83
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DB 62 SYOKSLGEADKADVNLTKAKSQ 84
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RESULT 14
US-09-879-257A-49
; Sequence 49, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-257A-49

Query Match 85.1%; Score 359; DB 9; Length 84;
Best Local Similarity 85.5%; Pred. No. 9.5e-36;

Search completed: October 9, 2003, 08:19:28
Job time : 155.851 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 36.5373 Seconds
(without alignments)
221.556 Million cell updates/sec

Title: US-09-928-048A-5

Perfect score: 253

Sequence: 1 FVALGAPLAPDAGSQRPRK.....KSLGEANKADVNLTKAKSQ 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	253	100.0	51	24	ABG74232
3	253	100.0	57	24	ABG74237
4	253	100.0	78	24	ABG74233
5	253	100.0	82	21	AAB07465
6	253	100.0	82	24	ABG74231
7	253	100.0	83	24	ABG74230
8	253	100.0	84	21	AAB07464
9	253	100.0	84	24	ABG74234

10	248	98.0	51	18	AAW08107	Human parathyroid PTH-(29-84). Synt
11	248	98.0	55	12	AAAR11732	hPTH mutin lackin
12	248	98.0	78	14	AAAR30852	Leu8 hPTH (7-84) m
13	248	98.0	78	14	AAAR30859	Human parathyroid
14	248	98.0	78	23	AAE23725	Parathyroid hormon
15	248	98.0	78	23	AAU73024	hPTH mutin lackin
16	248	98.0	79	14	AAAR30853	hPTH mutin lackin
17	248	98.0	80	14	AAAR35232	Parathyroid hormon
18	248	98.0	81	14	AAAR30854	Human PTH encoded
19	248	98.0	84	13	AAAR23790	Oxidation resistan
20	248	98.0	84	13	AAAR25571	Oxidation resistan
21	248	98.0	84	13	AAAR28845	Oxidation resistan
22	248	98.0	84	13	AAAR28846	Oxidation resistan
23	248	98.0	84	13	AAAR28847	Oxidation resistan
24	248	98.0	84	13	AAAR28848	Oxidation resistan
25	248	98.0	84	13	AAAR29561	Oxidation resistan
26	248	98.0	84	13	AAAR29562	Oxidation resistan
27	248	98.0	84	13	AAAR29563	Oxidation resistan
28	248	98.0	84	13	AAAR29564	Oxidation resistan
29	248	98.0	84	13	AAAR29565	Oxidation resistan
30	248	98.0	84	13	AAAR29566	Oxidation resistan
31	248	98.0	84	13	AAAR29567	Oxidation resistan
32	248	98.0	84	13	AAAR29568	Oxidation resistan
33	248	98.0	84	14	AAAR30860	Leu8 hPTH mutin
34	248	98.0	84	14	AAAR30857	Leu8 hPTH mutin
35	248	98.0	84	14	AAAR42067	Human parathyroid
36	248	98.0	84	14	AAAR42068	Stability-enhanced
37	248	98.0	84	14	AAAR42069	Stability-enhanced
38	248	98.0	84	14	AAAR42070	Stability-enhanced
39	248	98.0	84	14	AAAR42071	Stability-enhanced
40	248	98.0	84	14	AAAR42072	Stability-enhanced
41	248	98.0	84	14	AAAR42073	Stability-enhanced
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ALIGNMENTS

RESULT 1

AAB07466

ID AAB07466 standard; protein; 51 AA.

AC AAB07466;

XX 20-OCT-2000 (first entry)

DT 20-OCT-2000 (first entry)

DE Amino acid sequence of human parathyroid hormone antagonist.

XX Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.

XX Homo sapiens.

XX WO200042437-A1.

XX 20-JUL-2000.

XX 13-JAN-2000; 2000WO-US00855.

XX 14-JAN-1999; 99US-0231422.

XX 26-JUN-1999; 99US-0344639.

XX (SCAN-) SCANTIBODIES LAB INC.

XX WPI; 2000-476147/41.

PT Differentiating between normal parathyroid function and

PT hyperparathyroidism comprises determining and comparing whole

PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment

PT and/or total parathyroid hormone levels -

XX

AC ABG74233;
 XX
 DT 15-APR-2003 (first entry)
 XX
 DE Human parathyroid hormone-based CIP, PTH28-84 #1.
 XX
 KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
 XX CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 KW hypercalcaemia; osteosarcoma; extracellular calcium; PTH28-84.
 XX
 OS Homo sapiens.
 XX
 XX US2002160945-A1.
 PN
 PD 31-OCT-2002.
 XX
 XX 10-AUG-2001; 2001US-0928047.
 PF
 XX 10-AUG-2000; 2000US-224446P.
 PR
 XX (CANTOR/) CANTOR T L.
 PA
 PI Cantor TL;
 XX
 DR WPI; 2003-209227/20.
 XX
 PT Treating a patient having osteoporosis and is being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 XX
 PS Claim 2; Page 4; 8pp; English.
 XX
 CC The invention relates to treating a patient having osteoporosis
 CC comprising administering a cyclase inhibiting parathyroid hormone peptide
 CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
 CC hormone (PTH, which regulates extracellular calcium levels) antagonist
 CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
 CC the patient resulting from the administration of CAP. The peptide
 CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as
 CC -ABG74233). The present sequence is the CIP PTH28-84.
 CC Note: This peptide is referred to in the specification as PTH28-34
 CC but actually represents amino acids 7-84 of PTH. It is therefore unclear
 CC whether this peptide (SEQ ID 4) or the peptide appearing as ABG74237
 CC (which does represent amino acids 28-84 of PTH) is actually intended to
 CC be claimed.
 XX
 SQ Sequence 78 AA;
 XX
 Query Match 100.0%; Score 253; DB 24; Length 78;
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51
 Db 28 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 78
 RESULT 5
 AAB07465
 ID AAB07465 standard; protein; 82 AA.
 XX
 AC AAB07465;
 XX
 XX 20-OCT-2000 (first entry)
 DT
 XX Amino acid sequence of human parathyroid hormone antagonist.
 DE
 XX Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
 KW
 XX Homo sapiens.
 OS
 XX WO2000042437-A1.
 PN
 XX

PD 20-JUL-2000.
 XX
 PF 13-JAN-2000; 2000NO-US00855.
 XX
 PR 14-JAN-1999; 99US-0231422.
 PR 26-JUN-1999; 99US-0344639.
 XX
 PA (SCAN-) SCANTIBODIES LAB INC.
 XX
 DR WPI; 2000-476147/41.
 XX
 PT Differentiating between normal parathyroid function and
 PT hyperparathyroidism comprises determining and comparing whole
 PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
 PT and/or total parathyroid hormone levels -
 XX
 XX Disclosure; Page 42-43; 46pp; English.
 XX
 CC The present sequence represents a fragment of human parathyroid
 CC hormone (PTH), comprising residues 3-84, which functions as a PTH
 CC antagonist. The specification describes a method for differentiating
 CC between a person having substantially normal parathyroid function
 CC and having hyperparathyroidism. The method comprises determining and
 CC comparing at least two of the following parameters: whole parathyroid
 CC hormone level, parathyroid hormone inhibitory peptide fragment level
 CC and total parathyroid hormone level. The method is used for monitoring
 CC (treatments of) parathyroid related bone disease and the effects of
 CC therapeutic treatment for hyperparathyroidism.
 XX
 SQ Sequence 82 AA;
 XX
 Query Match 100.0%; Score 253; DB 21; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.7e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51
 Db 32 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 82
 RESULT 6
 ABG74231
 ID ABG74231 standard; peptide; 82 AA.
 XX
 AC ABG74231;
 XX
 DT 16-APR-2003 (first entry)
 DT
 XX Human parathyroid hormone-based CIP, PTH34-84.
 DE
 XX Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
 KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 KW hypercalcaemia; osteosarcoma; extracellular calcium; PTH34-84.
 XX
 OS Homo sapiens.
 XX
 PN US2002160945-A1.
 XX
 PD 31-OCT-2002.
 XX
 XX 10-AUG-2001; 2001US-0928047.
 PF
 XX 10-AUG-2000; 2000US-224446P.
 PR
 XX (CANTOR/) CANTOR T L.
 PA
 PI Cantor TL;
 XX
 DR WPI; 2003-209227/20.
 XX
 PT Treating a patient having osteoporosis and is being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 XX

XX PS Claim 1; Page 3; 8pp; English.

XX CC The invention relates to treating a patient having osteoporosis

XX CC comprising administering a cyclase inhibiting parathyroid hormone peptide

XX CC (CIP) or its conservatively substituted variant exhibiting a parathyroid

XX CC hormone (PTH, which regulates extracellular calcium levels) antagonist

XX CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in

XX CC the patient resulting from the administration of CAP. The peptide

XX CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230

XX CC -ABG74233). The present sequence is the CIP PTH34-84.

XX SQ Sequence 82 AA;

Query Match 100.0%; Score 253; DB 24; Length 82;

Best Local Similarity 100.0%; Pred. No. 1.7e-26;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

DB 32 FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 82

RESULT 7

ABG74230

ID ABG74230 standard; peptide; 83 AA.

XX AC ABG74230;

XX DT 16-APR-2003 (first entry)

XX DE Human parathyroid hormone-based CIP, PTH2-84.

XX KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;

XX KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;

XX KW hypercalcaemia; osteosarcoma; extracellular calcium; PTH2-84.

XX OS Homo sapiens.

XX PN US2002160945-A1.

XX PD 31-OCT-2002.

XX PF 10-AUG-2001; 2001US-0928047.

XX PR 10-AUG-2000; 2000US-224446P.

XX PA (CANT/) CANTOR T L.

XX PI Cantor TL;

XX DR WPI; 2003-209227/20.

XX PT Treating a patient having osteoporosis and is being administered

XX PT cyclase activating parathyroid hormone or its analogue comprises

XX PT administering a cyclase inhibiting parathyroid hormone peptide.

XX PS Claim 1; Page 3; 8pp; English.

XX CC The invention relates to treating a patient having osteoporosis

XX CC comprising administering a cyclase inhibiting parathyroid hormone peptide

XX CC (CIP) or its conservatively substituted variant exhibiting a parathyroid

XX CC hormone (PTH, which regulates extracellular calcium levels) antagonist

XX CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in

XX CC the patient resulting from the administration of CAP. The peptide

XX CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as

XX CC -ABG74233). The present sequence is the CIP PTH2-84.

XX SQ Sequence 83 AA;

Query Match 100.0%; Score 253; DB 24; Length 83;

Best Local Similarity 100.0%; Pred. No. 1.7e-26;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

DB 33 FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 83

RESULT 8

ABG07464

ID AAB07464 standard; protein; 84 AA.

XX AC AAB07464;

XX DT 20-OCT-2000 (first entry)

XX DE Amino acid sequence of human parathyroid hormone.

XX KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.

XX OS Homo sapiens.

XX PN WO200042437-A1.

XX PD 20-JUL-2000.

XX PE 13-JAN-2000; 2000WO-US00855.

XX PR 14-JAN-1999; 99US-0231422.

XX PR 26-JUN-1999; 99US-0344639.

XX PA (SCAN-) SCANTIBODIES LAB INC.

XX DR WPI; 2000-476147/41.

XX PT Differentiating between normal parathyroid function and

XX PT hyperparathyroidism comprises determining and comparing whole

XX PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment

XX PT and/or total parathyroid hormone levels.

XX PS Disclosure; Fig 1; 46pp; English.

XX CC The present sequence represents a human parathyroid hormone (PTH).

XX CC Fragments of PTH function as PTH antagonists. The specification

XX CC describes a method for differentiating between a person having

XX CC substantially normal parathyroid function and having hyperparathyroidism.

XX CC The method comprises determining and comparing at least two of the

XX CC following parameters: whole parathyroid hormone level, parathyroid

XX CC hormone inhibitory peptide fragment level and total parathyroid hormone

XX CC level. The method is used for monitoring (treatments of) parathyroid

XX CC related bone disease and the effects of therapeutic treatment for

XX CC hyperparathyroidism.

XX SQ Sequence 84 AA;

Query Match 100.0%; Score 253; DB 21; Length 84;

Best Local Similarity 100.0%; Pred. No. 1.8e-26;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

DB 34 FVALGAPLAPRDAGSQPRKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 84

RESULT 9

ABG74234

ID ABG74234 standard; peptide; 84 AA.

XX AC ABG74234;

XX DT 16-APR-2003 (first entry)

XX DE Human full length parathyroid hormone.

XX KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;

KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 KW hypercalcaemia; osteosarcoma; extracellular calcium.
 OS Homo sapiens.
 XX US2002160945-A1.
 PN 31-OCT-2002.
 PD 10-AUG-2001; 2001US-0928047.
 XX 10-AUG-2000; 2000US-224446P.
 PR (CANTOR) CANTOR T L.
 PA Cantor TL;
 PI WPI; 2003-209227/20.
 XX
 DR Treating a patient having osteoporosis and its being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 XX Disclosure; Fig 1; 8pp; English.
 PS The invention relates to treating a patient having osteoporosis
 XX comprising administering a cyclase inhibiting parathyroid hormone peptide
 CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
 CC hormone (PTH, which regulates extracellular calcium levels) antagonist
 CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
 CC the patient resulting from the administration of CAP. The peptide
 CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230
 CC -ABG74233). The present sequence is full length human PTH, the sequence
 CC upon which the CIP peptides are based.
 XX
 SQ Sequence 84 AA;
 Query Match 100.0%; Score 253; DB 24; Length 84;
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FVALGAPLAPDAGSQRPKKEDNVLSVESHEKSLGEANKADNVNLTAKSQ 51
 Db 34 FVALGAPLAPDAGSQRPKKEDNVLSVESHEKSLGEANKADNVNLTAKSQ 84
 RESULT 10
 AAW08107
 ID AAW08107 standard; peptide; 51 AA.
 XX
 AC AAW08107;
 XX 10-OCT-1997 (first entry)
 DT Human parathyroid hormone residues 34-84.
 DE Human; parathyroid hormone; PTH; CAMP-producing activity;
 KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
 KW climacteric disturbance.
 XX Synthetic.
 OS EP748817-A2.
 PN 18-DEC-1996.
 PD 13-JUN-1996; 96EP-0109475.
 XX 15-JUN-1995; 95JP-0148652.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX WPI; 1997-036114/04.
 DR New parathyroid hormone derivs. - useful in treatment of bone
 XX diseases, hypoparathyroidism and hypertension
 PT Claim 3; Page 39; 42pp; English.
 XX
 CC The sequences given in AAW08103-07 represent fragments of human para-
 CC thyroid hormone (PTH) which were used as Xaa34 in the generic sequence
 CC given in AAW08102. Peptides based on the generic sequence are human PTH
 CC (1-34) derivative peptides. They have potent CAMP-producing activity and
 CC bone formation activity. They may be used in treatment of bone
 CC diseases including osteoporosis, hypoparathyroidism, hypertension
 CC and climacteric disturbance. The peptides are low in toxicity and
 CC are safe.
 XX
 SQ Sequence 51 AA;
 Query Match 98.0%; Score 248; DB 18; Length 51;
 Best Local Similarity 98.0%; Pred. No. 4.5e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FVALGAPLAPDAGSQRPKKEDNVLSVESHEKSLGEANKADNVNLTAKSQ 51
 Db 1 FVALGAPLAPDAGSQRPKKEDNVLSVESHEKSLGEANKADNVNLTAKSQ 51
 RESULT 11
 AAR11732
 ID AAR11732 standard; Protein; 55 AA.
 XX
 AC AAR11732;
 XX 25-MAR-2003 (updated)
 DT 03-JUL-1991 (first entry)
 DE PTH-(29-84).
 KW Parathyroid hormone; calcium; osteoporosis; bone.
 XX Synthetic.
 OS WO9105050-A.
 PN 18-APR-1991.
 PD 01-OCT-1990; 90WO-C000335.
 PF 29-SEP-1989; 89CA-0615001.
 PR (CANA) NAT RES COUNCIL CANADA.
 PA Sung WL;
 PI WPI; 1991-132857/18.
 DR N-PSDB; AAQ11618.
 XX Mature human parathyroid synthesis - includes using eg E. coli
 PT transformed by plasmid contg. synthetic nucleotide sequence contg.
 PT adenine rich codons in N-terminal region.
 XX Disclosure; Fig 6; 62pp; English.
 PS Codons 29-84 are degenerate in the usage frequency favoured by
 CC E.coli or yeast. Codons 1-28 (see AAQ11617) are designed to contain
 CC adenine rich codons. The sequence is prepd. from eight oligo-
 CC nucleotides (4 on each strand). A plasmid contg. the complete
 CC sequence expresses PTH with an improved yield. PTH is a blood
 CC calcium regulator known to increase bone mass.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

XX PF 05-OCT-2001; 2001WO-US31082.
 XX PR 06-OCT-2000; 2000US-238134P.
 XX PR (HOLLI) HOLICK M F.
 PA Hollick MF;
 PI WPI: 2002-452304/48.
 DR N-PSDB; AAD37995.
 DR XX Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein -
 XX Claim 35; Fig 15; 56pp; English.
 PS The invention relates to a method for regulating proliferation or
 XX enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX Sequence 78 AA;
 SQ Query Match 98.0%; Score 248; DB 23; Length 78;
 Best Local Similarity 98.0%; Pred. No. 7.6e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGKANKADYNVLTAKSQ 51
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGKANKADYNVLTAKSQ 78
 RESULT 15
 AAU73024
 ID AAU73024 standard; peptide; 78 AA.
 AC AAU73024;
 XX 12-MAR-2002 (first entry)
 DT Parathyroid hormone PTH/PTHrP modulating domain #6.
 DE Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 OS Homo sapiens.
 XX WO200181415-A2.
 PN 01-NOV-2001.
 PD 27-APR-2001; 2001WO-US13528.

PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-265673P.
 PR 26-APR-2001; 2001US-0843221.
 XX (ANGE-) AMGEN INC.
 PA Kostenuik P, Liu C, Lacey DL;
 PI WPI: 2002-066435/09..
 DR Composition; useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX Disclosure; Page 26; 107pp; English.
 PS The invention relates to a composition (I) comprising modulators of
 XX parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX Sequence 78 AA;
 SQ Query Match 98.0%; Score 248; DB 23; Length 78;
 Best Local Similarity 98.0%; Pred. No. 7.6e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGKANKADYNVLTAKSQ 51
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGKANKADYNVLTAKSQ 78
 Search completed: October 9, 2003, 08:10:46
 Job time : 38.0373 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 18.2687 Seconds
(without alignments)
268.471 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSQRPK.....KSLGANKADNVNLTAKSQ 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	248	98.0	115 1 PTHU	parathyroid hormon
2	206	81.4	115 2 JC4202	parathyroid hormon
3	199	78.7	115 1 PTPBO	parathyroid hormon
4	194	76.7	115 1 PTPG	parathyroid hormon
5	160	63.2	105 2 I51851	parathyroid hormon
6	160	63.2	115 2 A05091	parathyroid hormon
7	68.5	27.1	119 2 A34937	parathyroid hormon
8	65	25.7	283 2 H86803	parathyroid hormon
9	63.5	25.1	487 2 A71407	prophage p13 prote
10	63	24.9	1937 2 I38055	probable Ste20-lik
11	61.5	24.3	366 2 A64028	myosin heavy chain
12	61	24.1	565 2 G89813	hypothetical prote
13	60.5	23.9	555 2 T44010	DNA polymerase III
14	60	23.7	258 2 A02985	virion protein Iim
15	60	23.7	955 2 S24348	myosin heavy chain
16	60	23.7	1938 2 A59293	myosin heavy chain
17	60	23.7	1940 2 A29320	skeletal myosin he
18	60	23.7	5170 2 T15348	myosin heavy chain
19	59.5	23.5	1400 2 T33758	hypothetical prote
20	59	23.3	404 2 C64597	lipopolysaccharide
21	58.5	23.1	142 2 T45922	probable C2H2-type
22	58	22.9	234 2 S33732	myosin alpha heavy
23	58	22.9	465 2 A02986	myosin alpha heavy
24	58	22.9	1038 1 MWRBCB	myosin beta heavy
25	58	22.9	1935 1 A71102	myosin beta heavy
26	58	22.9	1935 1 S06006	myosin beta heavy
27	58	22.9	1935 1 A59286	myosin heavy chain
28	57.5	22.7	378 2 F56653	virion protein - h
29	56.5	22.3	655 2 C71438	hypothetical prote

ALIGNMENTS

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: parathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Pott

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: GB:J00301; MID:g190702; PIDN:AA60215.1; PID:g190704

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid ho

A:Reference number: S53790; MUID:95225988; PMID:7710697

A:Accession: S53790

A:Molecule type: protein

A:Residues: 'X', 33, 'X', 35-46:65-84:105-110 <VAM>

A:Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human parathyroid hormone by a new microsequer

A:Reference number: A93169; MUID:74174967; PMID:4833516

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gauti

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylate

ation.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114, 'N' <OLS>

A:Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycos

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan,

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parat

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal res

A:Reference number: A93783; MUID:73070429; PMID:4509319

A:Accession: A93783

A:Molecule type: protein

hypothetical prote
hypothetical prote
DNA-damage repair
hypothetical prote
slow myosin heavy
myosin heavy chain
hypothetical prote
DNA-binding protei
hypothetical prote
neurofilament trip
neurofilament trip
disacylglycerol kin
hypothetical prote
synaptonemal compl
probable purine nu
myosin heavy chain

30 56.5 22.3 674 2 B71438
31 56.5 22.3 727 2 T24284
32 56 22.1 396 2 G96934
33 56 22.1 1787 2 G97222
34 56 22.1 1931 2 A59234
35 56 22.1 1938 1 JX0178
36 55.5 21.9 412 2 T51080
37 55.5 21.9 1203 2 S26650
38 55 21.7 269 2 T15500
39 55 21.7 854 2 S02003
40 55 21.7 1072 1 A37221
41 55 21.7 1154 2 T18525
42 55 21.7 1157 2 T19187
43 55 21.7 1505 2 T1418
44 55 21.7 1518 2 S37928
45 55 21.7 1934 2 I48153

A:Residues: 32-52, 'Q', 54-58, 'K', 60, 'L', 62-65 <BRE>
A:Note: This sequence was determined by sequenator and mass spectroscopic identification
R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A:Reference number: A90387; MUID:75146516; PMID:1125201
A:Accession: A90387
A:Molecule type: protein
A:Residues: 52-75 <KE3>
R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A:Title: Complete amino acid sequence of human parathyroid hormone.
A:Reference number: A90426; MUID:79082855; PMID:728431
A:Accession: A90426
A:Molecule type: protein
A:Residues: 61-106, 'D', 108-115 <KEU>
R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-14
A:Reference number: A94410
A:Accession: A94410
A:Molecule type: protein
A:Residues: 75-100 <KE2>
R:Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.
Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.
A:Reference number: A91660; MUID:75059220; PMID:4474131
A:Contents: annotation; synthesis of residues 32-65
A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were synthesized at renal adenylate cyclase assay and with the bovine hormone's active region in the child
R:Andreata, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, B.; Riniker, B.; Rittel, Hely. Chlm. Acta 56, 470-473, 1973
A:Title: Synthese der Sequenz 1-34 von menschlichem Parathormon.
A:Reference number: A91635; MUID:73227467; PMID:4721748
A:Contents: annotation; synthesis of residues 32-65
A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A:Reference number: I38342; MUID:82150870; PMID:6950361
A:Accession: I38342
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-115 <RES>
A:Cross-references: EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID:g37144
C:Genetics:
A:Gene: GDB:PTH
A:Cross-references: GDB:119522; OMIM:168450
A:Map position: 11p15.2-11p15.1
A:Introns: 29/2
A:Note: the first intron occurs before the initiator codon
C:Function:
A:Description: factor in homeostatic control of plasma calcium and phosphate; released & counter to calcitonin
C:Superfamily: parathyroid hormone; parathyroid hormone homology
C:Keywords: calcium; hormone; parathyroid gland; plasma
F:1-25/Domain: signal sequence \$status predicted <SIG>
F:26-31/Domain: propeptide \$status experimental <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-115/Product: parathyroid hormone \$status experimental <MAT>

Query Match 98.0%; Score 248; DB 1; Length 115;
Best Local Similarity 98.0%; Pred. No. 7e-23;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPDAGSORPRKEDNVLVSHEKSLGAEKADNVNLTAKSQ 51
DB 65 FVALGAPLAPDAGSORPRKEDNVLVSHEKSLGAEKADNVNLTAKSQ 115

RESULT 2
JC4202
parathyroid hormone precursor - dog

A:Reference number: A93776; MUID:71091588; PMID:4322265
 A:Contents: annotation; synthesis of residues 32-65
 A>Note: the synthetic peptide was active in vivo and in vitro
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
 Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 R:Weaver, C.A.; Gordon, D.F.
 Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
 A:Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' end of the parathyroid hormone gene
 A:Reference number: I45975; MUID:82037785; PMID:6170060
 A:Accession: I45975
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE2>
 A:Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643
 R:Weaver, C.A.; Gordon, D.F.
 Mol. Cell. Endocrinol. 28, 411-424, 1982
 A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
 A:Reference number: I45976; MUID:83105964; PMID:6185374
 A:Accession: I45976
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE3>
 A:Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
 C:Genetics:
 A:Gene: PTH
 A:Introns: 29/2
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Domain: parathyroid hormone #status experimental <MAT>
 Query Match 78.7%; Score 199; DB 1; Length 115;
 Best Local Similarity 80.4%; Pred. No. 6e-17;
 Matches 41; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVSHESKSLGAEKADNVNLTAKSQ 51
 DB 65 FVALGASIVRDGSSORPRKKEDNVLVSHESKSLGAEKADNVNLTAKSQ 115
 RESULT 4
 PTPG
 parathyroid hormone precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C:Accession: B26806; A90390; A90376; A01535
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
 Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone
 A:Reference number: A26806; MUID:87316938; PMID:3628009
 A:Accession: B26806
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-115 <SCH>
 A:Cross-references: GB:X05722; GB:X00409; NID:g1838; PIDN:CAA29193.1; PID:g1839
 R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
 Biochemistry 14, 3631-3635, 1975
 A:Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence
 A:Reference number: A90390; MUID:76018954; PMID:1164500
 A:Accession: A90390
 A:Molecule type: protein
 A:Residues: 26-115 <CHU>
 R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J.
 Biochemistry 13, 1994-1999, 1974
 A:Title: The amino acid sequence of porcine parathyroid hormone.
 A:Reference number: A90376; MUID:74253317; PMID:4840833
 A:Accession: A90376

A:Molecule type: protein
 A:Residues: 32-109 <SAD>
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
 Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Domain: parathyroid hormone #status experimental <MAT>
 Query Match 76.7%; Score 194; DB 1; Length 115;
 Best Local Similarity 78.4%; Pred. No. 2.4e-16;
 Matches 40; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVSHESKSLGAEKADNVNLTAKSQ 51
 DB 65 FVALGASIVRDGSSORPRKKEDNVLVSHESKSLGAEKADNVNLTAKSQ 115
 RESULT 5
 IS1851
 parathyroid hormone - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: IS1851
 R:Schmelzer, H.
 Adv. Gene Technol. 21, 228-229, 1984
 A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone
 A:Reference number: IS1851
 A:Accession: IS1851
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-105 <RES>
 A:Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933
 C:Genetics:
 A:Gene: PTH
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:20-54/Domain: parathyroid hormone homology <PTH>
 Query Match 63.2%; Score 160; DB 2; Length 105;
 Best Local Similarity 62.7%; Pred. No. 2.9e-12;
 Matches 32; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVSHESKSLGAEKADNVNLTAKSQ 51
 DB 55 FVSLGVQMAARESSVORPTKKEENVLDGNSKSLGEGDKADVDVLTAKSQ 105
 RESULT 6
 A05091
 parathyroid hormone precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
 C:Accession: A05091; A26806
 R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
 J. Biol. Chem. 259, 3320-3329, 1984
 A:Reference number: A05091; MUID:84135846; PMID:6321505
 A:Accession: A05091
 A:Molecule type: DNA
 A:Residues: 1-115 <HEI>
 A:Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
 A>Note: the authors translated the codon GAA for residue 87 as Asp
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
 Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone
 A:Reference number: A26806; MUID:87316938; PMID:3628009
 A:Accession: A26806
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA

A;Residues: 1-115 <SCH>
A;Cross-references: GB:X05721; GB:Y00409; NID:G56002; PIDN:CAA39192.1; PID:G56003
C;Genetics:
A;Introns: 29/3
C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;30-64/Domain: parathyroid hormone homology <PTH>

```
Query Match      63.2%; Score 160; DB 2; Length 115;
Best Local Similarity 62.7%; Pred. No. 3.2e-12;
Matches 32; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
```

Qy	1	FVALGAPLAPRDAGSQRP	KKXEDNVLV	SHESKSLG	EANKADV	NVLTKAKSQ	51
		:	:		:	:	:
		:	:		:	:	:
Db	65	FVSLGVMAAREGYSQRP	TKKENVLD	GNKSLG	EKGKADV	NVLVAKSQ	115
		:	:		:	:	:
		:	:		:	:	:

RESULT 7

A34937
parathyroid hormone precursor - chicken
C:Species: Gallus gallus (chicken)
C:date: 07-Sep-1990 #sequence_revision: 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: A34937; 150411
R:Russell, J.; Sherwood, L.M.
Mol. Endocrinol. 3, 325-331, 1989
A:title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone
A:Reference number: A34937; PMID:89219100; PMID:2710135

A;Accession: A34937
A;Molecule type: mRNA
A;Residues: 1-119 <RUS>
R;Cross-references: GB:IM31604; NID:g212767; PIDN:AAA49093.1; PID:g212768
R;Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.

J. Bone Miner. Res. 3, 689-698, 1988

A;Accession: I50411
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A:Residues: 1-119 <KHO>
A:Cross-references: GB:M36522; NID:g212591; PIDN:AB02866.1; PID:g212592
C:Superfamily: parathyroid hormone; parathyroid hormone homology
F:1-25/Domain: signal sequence \$status predicted <SIG>
F:26-31/Domain: propeptide \$status predicted <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-119/Product: parathyroid hormone \$status predicted <MAT>

Query Match 27.1%; Score 68.5; DB 2; Length 119;
Best Local Similarity 38.9%; Pred. No. 0.4;
Matches 21; Conservative 6; Mismatches 14; Indels 13; Gaps 1;

Qy 9 APRDAGSQRPRKKEDNVLE-----SHEKSLCEANKAD\NVLTAK 49
 | | | | | | | | : | : | : | | |
 Db 65 ALEDANTQRPKNKEDIVLGETLRNRRLPEHLRAAVOKKSIDDKAYNVLFCK 118

RESULT 8

H86803
 Prophage p13 protein 59 [Imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
 C:Species: *Lactococcus lactis* subsp. *lactis*
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: H86803
 R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissensbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A>Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
 A:Reference number: A86625; MUID:121235186; PMID:11337471

A;Accession: H86803
A;Status: preliminary
A;Molecule type: DNA

A:Residues: 1-283 <STO>
A:Cross-references: GB:AE005176; PDB:1272421; PTDN:AAK05530.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: pi359

Query Match 25.7%; Score 65; DB 2; Length 283;
Best Local Similarity 36.1%; Pred. No. 2.6;
Matches 13; Conservative 8; Mismatches .15; Indels

[illegible]

RESULT 9

probable Ste20-like kinase - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 A:Variety: columbiana
 C:date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 16-Dec-1998
 C:Accession: A71407
 R:Revan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergink
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weltzienegger, T.; Pohl, T.M.; Ter
 avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.;
 erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Recl
 C.: Chalwatzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from
A;Reference number: A71400: MIMD:98121113: PMID:9461215

A:Accession: A71407
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-487 <REV>
A:Cross-references: GB:297336; NID:g2244788; PID:e326893; PID:g2244804
C:Genetics:
A:Map position: 4COP9-4G3845
C:Superfamily: protein kinase homology
F:13-293/Domain: protein kinase homology <KIN>

Query Match	25.1%;	Score 63.5;	DB 2;	Length 487;
Best Local Similarity	30.2%;	Pred. No. 7.1;		

QY 9 APRDAGSQPRKKEDNVLVESHEKSLGEANKADNVLTAKSQ 51
:11: :1:111: :111: :11: :11:1
Db 374 SPREEDOSPKKEDDNNVITGYELGLSNE-----EAKNO 40

RESULT 10

I38055
 myosin heavy chain, perinatal skeletal muscle - human
 N; Contains: myosin ATPase (EC 3.6.4.1)
 C; Species: Homo sapiens (man)
 C; Date: 17-May-1996 #sequence revision 17-May-1996. #to
 C; Accession: I38055; J04154; SI2459; S09332; A0220; S
 R; Guilian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman
 Eur. J. Biochem. 230, 1001-1006, 1995
 A; Title: Characterization of a human perinatal myosin
 A; Reference number: I38055; MUID:95324556; PMID:760111

A;Accession: I38055
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-1937 <RES>
A/Cross-references: EMBL:Z38133; NID:q558668; PIDN:CAA86293.1; PTD:q558669
R;Karsch-Mizrachi, I.; Peghall, R.; Shows, T.B.; Leinward, L.A.
Gene 89, 289-294, 1990

A;Title: Generation of a full-length human perinatal myosin heavy-chain-encoding
A;Reference number: JH0154; MUID:90323631; PMID:2373371
A;Accession: JH0154
A;Molecule type: mRNA
A;Residues: 1-14, A',16-859 <K>
A;Cross-references: GB:Y00821
A;Experimental source: skeletal muscle
R;Bober, E.
submitted to the EMBL Data Library, January 1989
A;Reference number: S12458
A;Accession: S12459

A:Molecule type: mRNA
A:Residues: 502-1071, 'N', 1073-1250, 'DGG', 1253-1376, 'NT', 1379-1913, 'D', 1915-1937 <BOB>
A:Cross-references: EMBL:X51592; NID:g29465; PIDN:CAA35941.1; PID:g29466
A:Experimental source: clone gMHC-F
R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A:Title: Identification of three developmentally controlled isoforms of human myosin head
A:Reference number: S09331; MUID:90235862; PMID:1691980
A:Accession: S09332
A:Molecule type: mRNA
A:Residues: 502-547, 'X', 549-617, 'X', 619-687, 'X', 689-757, 'X', 759-827, 'X', 829-897, 'X', 899-1376, 'NT', 1379-1386, 'X', 1388-1456, 'X', 1458-1526, 'X', 1528-1596, 'X', 1598-1666, 'X', 1668-1717
A:Cross-references: EMBL:X51592
R:Peghail, R.; Leinwand, L.A.
J. Cell Biol. 108, 1791-1797, 1989
A:Title: Molecular genetic characterization of a developmentally regulated human perinatal myosin heavy chain
A:Reference number: A30220; MUID:89234168; PMID:2715179
A:Accession: A30220
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-1844
A:Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
C:Genetics:
A:Gene: GDB:MYH8
A:Cross-references: GDB:125267; OMIM:160741
A:Map position: 17pter-17p12
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide binding site
F:91-769/Domain: myosin motor domain homology <MYO>
F:181-188/Region: nucleotide-binding motif A (P-loop)
F:551-588/Region: actin binding #status predicted
F:658-680/Region: actin binding #status predicted
F:842-1282/Region: S2 #status predicted
F:698,708/Active site: Cys #status predicted

Query Match 24.9%; Score 63; DB 2; Length 1937;
Best Local Similarity 42.4%; Pred. No. 35;
Matches 14; Conservative 9; Mismatches 8; Indels 2; Gaps 1;
OY 21 KEDNVLSHEKSLG--EANKADNVLTAKSQ 51
DB 997 KEKALQTHQYLLDLDLQAEKDKVNLTKAKTK 1029

RESULT 11
A64028
hypothetical protein H11405 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: A64028
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervatage, P.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: A64028
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-366 <TIGR>
A:Cross-references: GB:U32820; GB:L42023; NID:g1574231; PIDN:AA23055.1; PID:g1574243; T

Query Match 24.3%; Score 61.5; DB 2; Length 366;
Best Local Similarity 35.6%; Pred. No. 9.1;
Matches 16; Conservative 10; Mismatches 18; Indels 1; Gaps 1;
OY 7 PLAPRDAGSQPRKKEDNVLSHEKSLGSEANKADNVLTAKSQ 51
DB 222 PTPKPKKKSEPNKKEDDYKELEKSL-KAKDEETQQLKDAQK 265

RESULT 12

G89813

DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (str)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89813
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 337, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-565 <KUR>
A:Cross-references: GB:BA000018; PID:g13700368; PIDN:BA841666.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: dnaX
C:Superfamily: DNA-directed DNA polymerase III gamma chain

Query Match 24.1%; Score 61; DB 2; Length 565;
Best Local Similarity 31.9%; Pred. No. 17;
Matches 15; Conservative 11; Mismatches 17; Indels 4; Gaps 1;
OY 3 ALGAPLAPRDAGSQPR---RKEDNVLSHEKSLGSEANKADNVLT 45
DB 391 AGGVSVAPQAQSSKKPARGIQKSNQAKVLDKANKADIKLL 437

RESULT 13
T44010
Varion protein [imported] - human herpesvirus 6
C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44010; T44197
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants
A:Reference number: 222732; MUID:99412319; PMID:10482554
A:Accession: T44010
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <ISE>
A:Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BA878271.1; PID:g4996038
A:Experimental source: strain HST; pop. variant B
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with
A:Reference number: 222734; MUID:99412318; PMID:10482553
A:Accession: T44197
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AAB06348.1
A:Experimental source: strain 229; variant B
C:Genetics:
A:Gene: US0
C:Superfamily: varicella-zoster virus gene 34 protein

Query Match 23.9%; Score 60.5; DB 2; Length 555;
Best Local Similarity 42.5%; Pred. No. 19;
Matches 17; Conservative 8; Mismatches 10; Indels 5; Gaps 2;
OY 16 QPRKKEDNVLSHEKSLGEA---NKADNVLTAKSQ 51
DB 67 QRKQKDSVLT-NSHLKAIEDALLFTNDGEVNVNTRADTQ 105

RESULT 14
A02985
myosin heavy chain, skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 13-Feb-1998

C/Accession: A02985

R:Capony, J.P.; Elzinga, M.

Biophys. J. 33, 148a, 1981

A:Reference number: A02985

A:Accession: A02985

A:Molecule type: protein

A:Residues: 1-258 <CAP>

A>Note: this fragment is from the heavy meromyosin subfragment-2

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

Query Match 23.7%; Score 60; DB 2; Length 258;
Best Local Similarity 42.4%; Pred. No. 9.6;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Oy 21 KEDNVLVESHEKSLG--EANKADYVNLTKAKSQ 51

|| | | | | | | | | | | | | | | | |

Db 152 KEKKALQEAHQOTLDDLOAEEDKVNTLTAKTK 184

RESULT 15

S24348

myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998

C/Accession: S24348

R:Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.

J. Mol. Biol. 225, 1143-1151, 1992

A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform

A:Reference number: S24348; MUID:92309413; PMID:1377278

A:Accession: S24348

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-955 <MOO>

A:Cross-references: EMBL:M74085

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match 23.7%; Score 60; DB 2; Length 955;
Best Local Similarity 42.4%; Pred. No. 38;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Oy 21 KEDNVLVESHEKSLG--EANKADYVNLTKAKSQ 51

|| | | | | | | | | | | | | | | | |

Db 13 KEKKALQEAHQOTLDDLOAEEDKVNTLTAKTK 45

Search completed: October 9, 2003, 08:14:29

Job time : 19.2687 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 9.89552 seconds
(without alignments)
242.368 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSORPRK.....KSLGEANKADVNLTKAKSQ 51

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	98.0	115	1 PTHY_HUMAN	P01270 homo sapien
2	241	95.3	115	1 PTH_MACFA	Q9xt35 macaca fasc
3	206	81.4	115	1 PTHY_CANFA	P52212 canis fami
4	199	78.7	115	1 PTHY_BOVIN	P01268 bos taurus
5	194	76.7	115	1 PTHY_PIG	P01269 sus scrofa
6	160	63.2	115	1 PTHY_RAT	P04089 rattus norv
7	68.5	27.1	119	1 PTHY_CHICK	P15743 gallus gall
8	63	24.9	1937	1 MYH8_HUMAN	P13535 homo sapien
9	61.5	24.3	366	1 YE05_HAEIN	P44180 haemophilus
10	60.5	23.9	555	1 UL25_HSV62	P52537 human herpe
11	60	23.7	1084	1 MYSS_RABIT	P02582 oryctolagus
12	60	23.7	1935	1 MYSS_CYPCA	Q90339 prinius ca
13	60	23.7	1938	1 MYH4_RABIT	Q28641 oryctolagus
14	60	23.7	1940	1 MYH3_CHICK	P02565 gallus gall
15	58.5	23.1	527	1 PTHY_RAT	P70486 rattus norv
16	58	22.9	465	1 MYH6_RABIT	P04460 oryctolagus
17	58	22.9	599	1 KLC2_MOUSE	O88448 mus musculu
18	58	22.9	1935	1 MYH7_HUMAN	P12883 homo sapien
19	58	22.9	1935	1 MYH7_PIG	P79293 sus scrofa
20	58	22.9	1935	1 MYH7_RAT	P02564 rattus norv
21	58	22.9	1939	1 MYH1_HUMAN	P12882 homo sapien
22	58	22.9	1941	1 MYH2_HUMAN	Q9ukx2 homo sapien
23	57.5	22.7	378	1 UL25_HSV6G	P52536 human herpe
24	57.5	22.7	555	1 UL25_HSV6U	P52387 human herpe
25	57	22.5	1939	1 MYH4_HUMAN	Q9y623 homo sapien
26	56	22.1	396	1 DPO4_CLOAB	Q97mb3 clostridium
27	56	22.1	1938	1 MYSS_CHICK	P13538 gallus gall
28	55.5	21.9	2426	1 SON_HUMAN	P18583 homo sapien
29	55	21.7	831	1 NFH_RAT	P16884 rattus norv
30	55	21.7	1154	1 KDGD_MESAU	O64398 mesocricetu
31	55	21.7	1505	1 SCP2_RAT	O70608 rattus norv
32	55	21.7	1518	1 KKK1_YEAST	P34244 saccharomyc
33	55	21.7	1934	1 MYH7_MESAU	P13540 mesocricetu

34	55	21.7	1938	1 MYH6_MOUSE	Q02566 mus musculu
35	55	21.7	1938	1 MYH6_RAT	P02563 rattus norv
36	55	21.7	1939	1 MYH6_MESAU	P13539 mesocricetu
37	54.5	21.5	587	1 GDA_ACFE	Q06700 acidaminoco
38	54	21.3	67	1 HARB_PYRAB	Q9v1f5 pyrococcus
39	54	21.3	67	1 HARB_PYRHO	O74092 pyrococcus
40	54	21.3	325	1 TDG_SCHPO	Q59825 schizosacch
41	54	21.3	622	1 KLC2_HUMAN	O9h0b6 homo sapien
42	54	21.3	736	1 MYH7_RABIT	P04461 oryctolagus
43	54	21.3	960	1 VP41_LYCES	P93231 lycopersico
44	54	21.3	983	1 PTPN_RAT	O63259 rattus norv
45	54	21.3	1033	1 Y328_MYCPN	P75310 mycoplasma

ALIGNMENTS

RESULT 1

ID	PTHY_HUMAN	STANDARD	PRT	115 AA
AC	P01270;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_taxid-9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	*Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.*;			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83169834; PubMed=6220408;			
RA	Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J.,			
RT	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RL	*Nucleotide sequence of the human parathyroid hormone gene.*;			
RN	[3]			
RP	SEQUENCE OF 26-37.			
RX	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	*Structural analysis of human parathyroid hormone by a new			
RL	microsequencing approach.*;			
RN	[4]			
RP	SEQUENCE OF 32-68.			
RX	MEDLINE=74111656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RT	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RL	*The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone.*;			
RN	[5]			
RP	SEQUENCE OF 61-83 AND 84-115.			
RX	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RT	Potts J.T. Jr.;			
RL	*Complete amino acid sequence of human parathyroid hormone.*;			
RN	[6]			
RP	SEQUENCE OF 75-100.			
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RT	O'Riordan J.L.H., Potts J.T. Jr.;			
RL	(In) Talmadge R.V., Owen M., Parsons J.A. (eds.);			
RN	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,			
RL	Amsterdam (1975).			

RP REVISIONS.
RX MEDLINE=75146516; PubMed=1125201;
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT "A reinvestigation of the amino-terminal sequence of human
RL parathyroid hormone."
RN Biochemistry 14:1842-1847(1975).
[8]
RP SYNTHESIS OF 32-65.
RX MEDLINE=75059220; PubMed=4474131;
RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
RA Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT "Solid-phase synthesis of the biologically active N-terminal 1-34
RL peptide of human parathyroid hormone."
RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
[9]
RP SYNTHESIS OF 32-65.
RX MEDLINE=73227467; PubMed=4721748;
RA Andreatta R.H., Hartmann A., Joehli A., Kamber B., Maier R.,
RA Riniker B., Rittell W., Sieber P.;
RT "Synthesis of sequence 1-34 of human parathyroid hormone."
RN Helv. Chim. Acta 56:470-473(1973).
[10]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE=91299748; PubMed=2069952;
RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT "Investigation of the solution structure of the human parathyroid
RL hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
RN and molecular dynamics calculations."
Biochemistry 30:6936-6942(1991).
[11]
RP STRUCTURE BY NMR OF 32-65.
RX MEDLINE=93345518; PubMed=8344299;
RA Barden J.A., Cuthbertson R.M.;
RT "Stabilized NMR structure of human parathyroid hormone(1-34).";
RN Eur. J. Biochem. 215:315-321(1993).
[12]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=95318084; PubMed=7797503;
RA Marx U.C., Austermann S., Bayer P., Ademann K., Eichert A.,
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA Roesch P.;
RT "Structure of human parathyroid hormone 1-37 in solution."
RN J. Biol. Chem. 270:15194-15202(1995).
[13]
RP STRUCTURE BY NMR OF 32-70.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Ademann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RN bPTH(1-37).";
Biochem. Biophys. Res. Commun. 267:213-220(2000).
[14]
RP VARIANT ARG-18.
RX MEDLINE=91009811; PubMed=2212001;
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA Kronenberg H.M.;
RT "Mutation of the signal peptide-encoding region of the
RL preproparathyroid hormone gene in familial isolated
RN hypoparathyroidism."
J. Clin. Invest. 86:1084-1087(1990).
CC -J- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -I- DISEASE: Defects in PTH are a cause of familial isolated
CC hypoparathyroidism (FHH) [MIM:146200].
CC -I- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC
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DR EMBL; J00301; AAA60215.1;
DR EMBL; V00597; CAA23843.1;
DR EMBL; A29146; CAA01956.1;
DR PIR; A19339; PTHU.
DR PDB; 1HPH; 10-JUL-95
DR PDB; 1HTH; 15-OCT-97
DR PDB; 1ZWA; 12-MAR-97
DR PDB; 1ZWB; 12-MAR-97
DR PDB; 1ZWD; 12-MAR-97
DR PDB; 1ZWE; 12-MAR-97
DR PDB; 1ZWF; 16-JUN-97
DR PDB; 1ZWG; 16-JUN-97
DR PDB; 1BWX; 14-JAN-00
DR PDB; 1HPY; 14-JAN-00
DR PDB; 1ET1; 06-SEP-00
DR PDB; 1ET2; 06-SEP-00
DR PDB; 1FVY; 31-DEC-02
DR Genew; HGNC:9606; PTH.
DR MIM; 168450;
DR MIM; 146200;
DR GO; GO:0008492; F:GMP generating peptide activity; TAS.
DR GO; GO:0005180; F:peptide hormone; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . TAS.
DR GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR001415; Parathyroid_hrm.
DR InterPro; IPR003625; Pthyro_hrm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR PRODOM; PD010687; Pthyro_hrm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal; Disease mutation; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18
FT
FT CONFLICT 107 107
FT HELIX 36 41
FT TURN 42 43
FT HELIX 49 63
FT TURN 64 66
SQ SEQUENCE 115 AA; 12861 MW; 849015736A6B5597 CRC64;
Query Match 98.0%; Score 248; DB 1; Length 115;
Best Local Similarity 98.0%; Pred. No. 1.9e-23;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 FVALGAPLAPDAGSQPRKKEDNVLVESKSLGEADKADNVNLTAKSQ 51
Dy 65 FVALGAPLAPDAGSQPRKKEDNVLVESKSLGEADKADNVNLTAKSQ 115
RESULT 2
PTH_MACFA STANDARD; PRT; 115 AA.
AC Q9XT35;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.

RA Malaivijitnond S., Takenaka O.;
 RT "Nucleotide sequences of parathyroid gene in five species of macaque
 RL of Thailand";
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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 CC -----
 DR EMBL; AF130257; RAD2777.1; -;
 DR HSPF; P01270; LHPY;
 DR InterPro; IPR001415; Parathyrd_hrm.
 DR InterPro; IPR003625; Pthyrdorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyrdorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;
 Query Match 95.3%; Score 241; DB 1; Length 115;
 Best Local Similarity 92.2%; Pred. No. 1.3e-22;
 Matches 47; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSQPRKKEDNVLSHEKSGLGEAKADVNLTKAKSQ 51
 Db 65 FVALGAPLAPRDAGSQPRKKEDNVLSHEKSGLGEAKADVNLTKAKSQ 115
 RESULT 3
 PTHY_CANFA
 ID PTHY_CANFA STANDARD; PRT; 115 AA.
 AC PS2212;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parathyroid;
 RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
 RA DeWille J.W., Capen C.C.;
 RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
 RT protein and parathyroid hormone";
 RL Gene 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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 CC -----

DR EMBL; U15662; AAA82584.1; -;
 DR PIR; JC4202; JC4202.
 DR HSPF; P01268; IZWC.
 DR InterPro; IPR001415; Parathyrd_hrm.
 DR InterPro; IPR003625; Pthyrdorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyrdorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; FC38F77FC8CFE56 CRC64;
 Query Match 81.4%; Score 206; DB 1; Length 115;
 Best Local Similarity 82.4%; Pred. No. 2.5e-18;
 Matches 42; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSQPRKKEDNVLSHEKSGLGEAKADVNLTKAKSQ 51
 Db 65 FVALGAPLAPRDAGSQPRKKEDNVLSHEKSGLGEAKADVNLTKAKSQ 115
 RESULT 4
 PTHY_BOVIN
 ID PTHY_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=80056617; PubMed=388425;
 RA Kronenberg H.M., McDavitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
 RA Potts J.T. Jr., Rich A.;
 RT "Cloning and nucleotide sequence of DNA coding for bovine
 RT preproparathyroid hormone";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82037785; PubMed=6170060;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Introduction by molecular cloning of artifactual inverted sequences
 RT at the 5' terminus of the sense strand of bovine parathyroid hormone
 RT cDNA";
 RL Mol. Cell. Endocrinol. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84262483; PubMed=6086460;
 RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
 RT "Isolation and complete nucleotide sequence of the gene for bovine
 RT parathyroid hormone";
 RL Gene 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE=74142666; PubMed=4522780;
 RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
 RA Cohn D.V.;
 RT "The N-terminal amino-acid sequence of bovine preparathyroid

[illegible]

RESULT 6

PTHY_RAT PTHY_RAT STANDARD; PRT; 115 AA.

AC P04089; 063473;

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Parathyroid hormone precursor (Parathyrin) (PTH).

GN PTH.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP MEDLINE-84135846; PubMed-6321505;

RX Heintz G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;

RA "Gene encoding parathyroid hormone. Nucleotide sequence of the rat gene and deduced amino acid sequence of rat preproparathyroid hormone.";

RT J. Biol. Chem. 259:3320-3329(1984).

RN [2]

RP MEDLINE-87316938; PubMed-3628009;

RX Schmelzer H.-J., Gross G., Widera G., Mayer H.;

RA "Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";

RT Nucleic Acids Res. 15:6740-6740(1987).

RN [3]

RP MEDLINE-10-115 FROM N.A.

RP TISSUE-Parathyroid;

RA Schmelzer H.-J., Gross G., Mayer H.;

RA "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.";

RT Adv. Gene Technol. 21:228-229(1984).

RN [4]

RP MEDLINE-9284968; PubMed-3251402;

RX Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr., Kronenberg H.M.;

RA "Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.";

RT J. Bone Miner. Res. 3:689-698(1988).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -1- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.

CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

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DR EMBL; K01268; AAA41979.1;

DR EMBL; X05721; CAA29192.1;

DR EMBL; M54875; AAA57156.1;

DR EMBL; S80127; -; NOT_ANNOTATED_CDS.

DR PIR; A05091; A05091.

DR HSP; P01270; 12WB.

DR InterPro; IPR001415; Parathyrd_hrm.

DR Pfam; P01279; Parathyrd_sub.

DR ProDom; PD010687; Pthyrdorm_sub.

DR SMART; SM00087; PTH; 1.

DR PROSITE; PS00335; PARATHYROID; 1.

KW Hormone; Signal.

FT SIGNAL 1 25

FT PROPEP 26 31

FT CHAIN 32 115 PARATHYROID HORMONE.

FT CHAIN 32 115 C -> Y (IN REF. 3).

FT CONFLICT 18 18

FT CONFLICT 23 23 A -> T (IN REF. 3).

FT CONFLICT 33 33 V -> I (IN REF. 3).

FT CONFLICT 62 62 V -> G (IN REF. 3).

SQ SEQUENCE 115 AA; 12722 MW; 7B434CFCFA528B230 CRC64;

Query Match 63.2%; Score 160; DB 1; Length 115;

Best Local Similarity 62.7%; Pred. No. 1e-12; Indels 0; Gaps 0;

Matches 32; Conservative 8; Mismatches 11;

OY 1 FVALGAPLAPRDAGSORPRKEDNVLVESHEKSLGSEKANKADVNVLTAKSQ 51

DB 65 FVSLGVQMAAREGSYQRTTKKEENVLDGNSKSLGEGDKADVDVLVAKSQ 115

RESULT 7

PTHY_CHICK PTHY_CHICK STANDARD; PRT; 119 AA.

AC P15743;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Parathyroid hormone precursor (PTH).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP MEDLINE-89219100; PubMed-2710135;

RX Russell J., Sherwood L.M.;

RA "Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone mRNA and the deduced sequence of the hormone precursor.";

RT Mol. Endocrinol. 3:325-331(1989).

RN [2]

RP MEDLINE-9284968; PubMed-3251402;

RX Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr., Kronenberg H.M.;

RA "Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.";

RT J. Bone Miner. Res. 3:689-698(1988).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

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DR EMBL; M31504; AAA49093.1;

DR EMBL; M36522; AAB02866.1;

DR PIR; A34937; A34937.

DR HSP; P01270; 1HPY.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyrdorm_sub.

DR Pfam; P01279; Parathyrd_sub.

DR ProDom; PD010687; Pthyrdorm_sub; 1.

DR SMART; SM00087; PTH; 1.

DR PROSITE; PS00335; PARATHYROID; 1.

KW Hormone; Signal.

FT SIGNAL 1 25

FT PROPEP 26 31

FT CHAIN 32 119 PARATHYROID HORMONE.

FT CHAIN 32 119

SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;

Query Match 27.1%; Score 68.5; DB 1; Length 119;

Best Local Similarity 38.9%; Pred. No. 0.16;


```
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H11405.
GN H11405.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512(1995).
CC -----
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CC -----
DR EMBL: U32820; AAC23055.1;
DR PIR: A64028; A64028.
DR TIGR: H11405;
DR KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 366 AA; 40122 MW; 6804080B631AEC0 CRC64;
Query Match 24.3%; Score 61.5; DB 1; Length 366;
Best Local Similarity 35.6%; Pred. No. 3.9;
Matches 16; Conservative 10; Mismatches 18; Indels 1; Gaps 1;
QY 7 PLAPRAGSORPRKEDNVLVESHEKSLGEAKADVNVLTAKSQ 51
Db 222 PTRPKERKSPENKEDDVEKELEKSL-KAKDEIQQLKDAQK 265
RESULT 10
UL25 HSV62
ID UL25_HSV62 STANDARD; PRT; 555 AA.
AC P52537;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Virion protein U50.
GN U50 OR Kall.
OS Human herpesvirus (type 6 / strain 229) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=36351;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95074921; PubMed=7983761;
RA Stanley F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
RT "Intragenomic linear amplification of human herpesvirus 6B orilyt
RT suggests acquisition of orilyt by transposition.";
RL J. Virol. 69:589-596(1995).
CC -1- FUNCTION: VIRION PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC HSV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC -----
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CC -----
DR EMBL: AF157706; AAB06348.1;
DR PIR: T44010; T44010.
DR InterPro: IPR002493; UL25.
DR Pfam: PF01499; UL25; 1.
SQ SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;
Query Match 23.9%; Score 60.5; DB 1; Length 555;
Best Local Similarity 42.5%; Pred. No. 8.3;
Matches 17; Conservative 8; Mismatches 10; Indels 5; Gaps 2;
QY 16 QRRPKEDNVLVESHEKSLGEA----NKADYVNVLTAKSQ 51
Db 67 QRKMQKSDVL-NSHLKRAIEDALLFTNDGEVNVETKADTQ 105
RESULT 11
MYSS_RABIT
ID MYSS_RABIT STANDARD; PRT; 1084 AA.
AC P02562;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Myosin heavy chain, skeletal muscle (Fragments).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE OF 1-258.
RA Capony J.-P., Elzinga M.;
RT "The amino acid sequence of a 34,000 dalton fragment from S-2 of
RL Biophys. J. 33:148A-148A(1981).
RN [2]
RP SEQUENCE OF 259-428.
RX MEDLINE=85131142; PubMed=3972832;
RA Lu R.C., Wong A.;
RT "The amino acid sequence and stability predictions of the hinge
RT region in myosin subfragment 2.";
RL J. Biol. Chem. 260:3456-3461(1985).
RN [3]
RP SEQUENCE OF 409-1084 FROM N.A.
RX MEDLINE=87304245; PubMed=3305014;
RA Maeda K., Szakiel G., Wittinghofer A.;
RT "Characterization of cDNA coding for the complete light meromyosin
RT portion of a rabbit fast skeletal muscle myosin heavy chain.";
RL Eur. J. Biochem. 167:97-102(1987).
CC -1- FUNCTION: MUSCLE CONTRACTION.
CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC -1- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES,
CC WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
CC CONSERVED.
CC -----
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 45.6716 Seconds
(without alignments)
288.159 Million cell updates/sec

Title: US-09-928-048a-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSQPRK.....KSLGEANKADVNLTKAKSQ 51

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	205	81.0	115	6 Q9GL67	Q9GL67 felis silve
2	203	80.2	86	6 Q9N1V0	Q9N1V0 equus caball
3	158	62.5	115	11 Q9ZOL6	Q9ZOL6 mus musculus
4	65	25.7	283	9 Q9AZW5	Q9AZW5 bacterioph
5	65	25.7	283	16 Q9CFN5	Q9CFN5 lactococcus
6	63.5	25.1	487	10 Q23304	Q23304 arabidopsis
7	63	24.9	975	13 Q98TQ5	Q98TQ5 notothenia
8	63	24.9	1119	13 P87344	P87344 theragra ch
9	63	24.9	1287	13 Q93498	Q93498 theragra ch
10	63	24.9	1299	13 Q98TQ6	Q98TQ6 notothenia
11	61	24.1	585	16 Q99WCS	Q99WCS staphylococ
12	60	23.7	1092	13 Q90338	Q90338 cyprinus ca
13	60	23.7	1930	13 Q90GDS	Q90GDS pennahia ar
14	60	23.7	1931	13 Q910C5	Q910C5 gallus gall
15	60	23.7	1931	13 Q42352	Q42352 cyprinus ca
16	60	23.7	1933	13 Q90337	Q90337 cyprinus ca

17	60	23.7	1936	13 Q90YF6	Q90YF6 paracirrh
18	60	23.7	1937	6 Q9TV62	Q9TV62 sus scrofa
19	60	23.7	1937	6 Q8MJV1	Q8MJV1 equus caball
20	60	23.7	1938	6 Q8MJV0	Q8MJV0 equus caball
21	60	23.7	1938	6 Q8BE40	Q8BE40 bos taurus
22	60	23.7	1938	13 Q9IBD7	Q9IBD7 seriola dum
23	60	23.7	1939	6 Q9TV63	Q9TV63 sus scrofa
24	60	23.7	1939	6 Q9TV61	Q9TV61 sus scrofa
25	60	23.7	1940	6 Q8BE41	Q8BE41 bos taurus
26	60	23.7	1940	13 Q8AY28	Q8AY28 gallus gall
27	60	23.7	1941	13 Q8DGM4	Q8DGM4 gallus gall
28	60	23.7	1943	13 Q8JG72	Q8JG72 gallus gall
29	60	23.7	1944	13 Q9DGM5	Q9DGM5 gallus gall
30	60	23.7	6994	5 Q17343	Q17343 caenorhabdi
31	59.5	23.5	909	2 Q52585	Q52585 pseudomonas
32	59.5	23.5	909	2 Q52585	Q52585 pseudomonas
33	59.5	23.5	1400	5 Q8TYW5	Q8TYW5 caenorhabdi
34	59	23.3	462	2 Q05090	Q05090 nocardioid
35	59	23.3	565	16 Q8NY08	Q8NY08 staphylococ
36	59	23.3	823	16 Q8PBY4	Q8PBY4 xanthomonas
37	59	23.3	1006	4 Q96157	Q96157 homo sapien
38	59	23.3	1889	4 Q9H430	Q9H430 homo sapien
39	59	23.3	2010	4 Q9P216	Q9P216 homo sapien
40	58.5	23.1	142	10 Q9M344	Q9M344 arabidopsis
41	58.5	23.1	288	10 Q94G09	Q94G09 oryza sativ
42	58	22.9	234	6 Q28829	Q28829 oryctolagus
43	58	22.9	258	4 Q92679	Q92679 homo sapien
44	58	22.9	518	5 Q9VRP4	Q9VRP4 drosophila
45	58	22.9	619	11 Q91Y54	Q91Y54 mus musculu

ALIGNMENTS

RESULT 1	Q9GL67	PRELIMINARY;	PRT;	115 AA.
ID	Q9GL67			
AC	Q9GL67			
DT	01-MAR-2001 (TREMREL. 16, Created)			
DT	01-MAR-2001 (TREMREL. 16, Last sequence update)			
DT	01-JUN-2002 (TREMREL. 21, Last annotation update)			
DE	Preproparathyroid hormone precursor.			
GN	PTH.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxID=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;			
RT	"Molecular cloning of feline preproparathyroid hormone."			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF309967; AAG30545.1;			
DR	HSSP; P01268; IWC.			
DR	InterPro; IPR001415; Parathyrd_hrm.			
DR	InterPro; IPR003625; Pthyrdorm_sub.			
DR	Pfam; PF01279; Parathyroid; 1.			
DR	ProDom; PD010687; Pthyrdorm_sub; 1.			
DR	SMART; SM000087; PTH; 1.			
DR	PROSITE; PS00335; PARATHYROID; 1.			
FT	SIGNAL			
FT	CHAIN			
FT	SEQUENCE			
FT	115 AA; 12921 MW; 80CD557CC6A1A47E CRC64;			

Query Match	81.0%;	Score	205;	DB	6;	Length	115;
Best Local Similarity	80.4%;	Pred. No.	3.6e-18;				
Matches	41;	Conservative	5;	Mismatches	5;	Indels	0;
Qy	1	FVALGAPLAPRDAGSQPRKEDNVLVESKSLGEANKADVNLTKAKSQ	51				
Db	65	FVALGAPLAPRDAGSQPRKEDNVPAENHQKSLGEANKADVNLTKAKSQ	115				

```
RESULT 2
Q9N1V0 PRELIMINARY; PRT; 86 AA.
ID Q9N1V0
AC Q9N1V0
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shiu Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134233; AAF62347.1; -
DR HSP; P01270; IHPY.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthythorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; pthythorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1
SQ SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;

Query Match 80.2%; Score 203; DB 6; Length 86;
Best Local Similarity 76.5%; Pred. No. 4.7e-18;
Matches 39; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 FVALGAPLADAGSQRPKRKEDNVLSHEKSLGSEANKADVNLTKAKSQ 51
DQ 36 FIALGAPFIRHGGSQRPKRKEDNVLSHEKSLGSEANKADVNLTKAKSQ 86

RESULT 3
Q9Z0L6 PRELIMINARY; PRT; 115 AA.
ID Q9Z0L6
AC Q9Z0L6
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Parathyroid hormone precursor.
GN PTH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RA Karaplis A.C., He B., Hsiao-Tim F.F.T., Al-Akad B., Kronenberg H.M.;
RT Cloning of the murine gene encoding parathyroid hormone: genomic
RT organization and nucleotide sequence.
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF066075; AAC99656.1; -
DR HSP; P01270; 12WB.
DR MGD; MGI:97799; Pth.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthythorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; pthythorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW SIGNAL.
FT CHAIN 1 25 POTENTIAL.
FT CHAIN 32 115 PARATHYROID HORMONE.
```

```
SQ SEQUENCE 115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;

Query Match 62.5%; Score 158; DB 11; Length 115;
Best Local Similarity 60.8%; Pred. No. 3.1e-12;
Matches 31; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 FVALGAPLADAGSQRPKRKEDNVLSHEKSLGSEANKADVNLTKAKSQ 51
DQ 65 FVSLGVQMAARDGSHQKPTKKEENVLDGNPKSLGEGDKADVNLVSKSQ 115

RESULT 4
Q9AZW5 PRELIMINARY; PRT; 283 AA.
ID Q9AZW5
AC Q9AZW5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Orf2.
GN ORF2.
OS Bacteriophage b11286.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=151536;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21113149; PubMed=11160885;
RA Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
RT "Analysis of six prophages in Lactococcus lactis IL1403: different
RT genetic structure of temperate and virulent phage populations.";
RL Nucleic Acids Res. 29:644-651(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF232659; AAK08289.1; -
SQ SEQUENCE 283 AA; 31164 MW; DF4094313735E02A CRC64;

Query Match 25.7%; Score 65; DB 9; Length 283;
Best Local Similarity 36.1%; Pred. No. 4.7;
Matches 13; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 15 SQRPKRKEDNVLSHEKSLGSEANKADVNLTKAKS 50
DQ 110 SKESKSDSNLLIDSOYKEADENGADSAVLVATKS 145

RESULT 5
Q9CFN5 PRELIMINARY; PRT; 283 AA.
ID Q9CFN5
AC Q9CFN5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Prophage p13 protein 59.
GN P1359 OR LLI432.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ILI403;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006373; AAK05530.1; -
KW Complete proteome.
SQ SEQUENCE 283 AA; 31164 MW; DF4094313735E02A CRC64;

Query Match 25.7%; Score 65; DB 16; Length 283;
Best Local Similarity 36.1%; Pred. No. 4.7;
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Matches 13; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
QY 15 SQRPKEKEDNVLVESHKSLGAEANKADNVNLTAKSQ 50
   : : : : : : : : : : : : : : : : : : : :
Db 110 SKESKSDSNLLIDSYKEIADENGADSAVLATKS 145
   : : : : : : : : : : : : : : : : : : : :

RESULT 6
O23304
ID O23304 PRELIMINARY; PRT; 487 AA.
AC O23304
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE STE20-like kinase homolog (Kinase like protein).
GN ATG14480
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,
RA Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme K., Ansgore W., Delsen M., Bancroft I., Mewes H.W.,
RA Schueller C., Chalvatzis N.,
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97336; CAB10227.1;
DR EMBL; AL161539; CAB78490.1;
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 487 AA; 54380 MW; 77D21D39D2FB4F20 CRC64;

Query Match 25.1%; Score 63.5; DB 10; Length 487;
Best Local Similarity 30.2%; Pred. No. 14;
Matches 13; Conservative 12; Mismatches 11; Indels 7; Gaps 1;
QY 9 APRDAGSQRPKEKEDNVLVESHKSLGAEANKADNVNLTAKSQ 51
   : : : : : : : : : : : : : : : : : : : :
Db 374 SPREDQSKDKEDDNTTGYELGLSLNE-----EAKNQ 409
   : : : : : : : : : : : : : : : : : : : :

RESULT 7
Q98T05
ID Q98T05 PRELIMINARY; PRT; 975 AA.
AC Q98T05
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myosin heavy chain (Fragment).
GN MYOHC-A3 GENE.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Nototheniidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RA Gauvry L., Ennion S., Ettelale C., Goldspink G.;
RT "Characterisation of red and white muscle myosin heavy chain gene

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coding sequences from Antarctic and tropical fish.";
RL Comp. Biochem. Physiol. 127:575-588(2000).
DR EMBL; AJ243768; CAC27777.1;
DR HSSP; P03437; IHTM.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR NON_TER 1
SQ SEQUENCE 975 AA; 112313 MW; 2F7AD46A3419537F CRC64;

Query Match 24.9%; Score 63; DB 13; Length 975;
Best Local Similarity 45.5%; Pred. No. 34;
Matches 15; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
QY 21 KEDNVLVESHKSLG--EANKADNVNLTAKSQ 51
   : : : : : : : : : : : : : : : : : : : :
Db 34 KEKALQESHQOTLDDLQAEEDKVNLTAKTK 66
   : : : : : : : : : : : : : : : : : : : :

RESULT 8
P87344
ID P87344 PRELIMINARY; PRT; 1119 AA.
AC P87344
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin heavy chain (Fragment).
OS Theragra chalcogramma (Alaska pollock).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast muscle;
RA Tozashi M., Hirayama Y., Kakimura M., Watabe S., Ojima T., Nishita K.;
RT "cDNA cloning of Alaska polack fast skeletal muscle myosin heavy
chain.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000214; BAA19070.1;
DR HSSP; P13538; 2MYS.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR NON_TER 1
SQ SEQUENCE 1119 AA; 128626 MW; B8C5FECAE6F5B954 CRC64;

Query Match 24.9%; Score 63; DB 13; Length 1119;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 15; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
QY 21 KEDNVLVESHKSLG--EANKADNVNLTAKSQ 51
   : : : : : : : : : : : : : : : : : : : :
Db 178 KEKALQESHQOTLDDLQAEEDKVNLTAKTK 210
   : : : : : : : : : : : : : : : : : : : :

RESULT 9
O93498
ID O93498 PRELIMINARY; PRT; 1287 AA.
AC O93498
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin heavy chain (Fragment).
OS Theragra chalcogramma (Alaska pollock).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.

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Matches   15; Conservative    7; Mismatches     9; Indels      2; Gaps       1;

QY          21 KEDNVLVESHKSLG--EANKADVNVLTAKSQ 51
              ||| ||||::: :|| ::|| ||||||:
DB         988 KERKALQESHQOTLDDIQAEEDKVNTLTRAKTK 1020


RESULT 11
Q99WC5      Q99WC5 PRELIMINARY; PRT; 565 AA.
ID AC
AC Q99WC5;
DT DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DI 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE DNA polymerase III gamma and tau subunits.
GN DNAX OR SAVO478 OR SA0436
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OC Staphylococcus aureus (Strain N315).
OX Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879; [1]
RN RN SEQUENCE FROM N.A.
RP RP SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RC MEDLINE=21311952; PubMed=11418146;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Liap J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaijo C.,
RA Sekimizu K., Hirakata H., Kohara S., Goto S., Yasubaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramoto K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus".
RL Lancet. 357:1225-1240(2001).
DR EMBL; AF003359; BAB56640.1; -
DR EMBL; AP009130; BAB41666.1; -
DR InterPro; IPRO03593; AAA_ATPase.
DR InterPro; IPRO03959; AAA_ATPase_centre.
DR InterPro; IPRO01270; Chaperlin_c1pA/B.
DR InterPro; IPRO00345; Cytc_heme_bind.
DR InterPro; IPRO00483; Fatty_acid_BP.
DR InterPro; IPRO00862; RFCDomain.
DR Pfam; PF00004; AAA; 1.
DR PRINTS; PR00300; CLPPRTPASEA.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00150; CYTCCHROME_C; 1.
DR PROSITE; PS00214; FABF; 1.
KW Complete proteome.
SQ SEQUENCE 565 AA; 63471 MW; F29A7F07095F02AA CRC64;

Query Match             24.1%; Score 61; DB 16; Length 565;
Best Local Similarity   31.9%; Pred.No. 33;
Matches 15; Conservative 11; Mismatches 17; Indels 4; Gaps 1;

QY           3 ALGAPLAPRDAGSORP-----RKKEINVLESHEKSIGLEANKADVNL 45
              ||| |||| :|| :|| ::|| ||||||:
DB        391 AQGVSVAPAQSCKSPARGCIQRKNAFSMQQIAKLVDXNKADIKLL 437


RESULT 12
Q90338      Q90338 PRELIMINARY; PRT; 1092 AA.
ID AC
AC Q90338;
DT DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DI 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Myosin heavy chain (Fragment).
GN OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Actinopterygii; Neoplatygil; Teleostei; Ostariophysi; Cypriniformes;
CYPRINIDAE; Cyprinus. NCBI_TaxID=7962;
RN RN
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RP SEQUENCE FROM N.A.
RC TISSUE-Fast muscle;
RX MEDLINE-97176447; PubMed-9023999;
RA Inai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT muscle and their gene expression associated with temperature
RL J. Exp. Biol. 200:27-34(1997).
DR EMBL: D50475; BAA09068.1; -.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF01576; Myosin_tail; 1.
FT NON_TER 1
SQ SEQUENCE 1092 AA; 125885 MW; B6BABA3963BEEBA CRC64;

Query Match 23.7%; Score 60; DB 13; Length 1092;
Best Local Similarity 42.4%; Pred. No. 94;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

OY 21 KEDNVLVESHEKSLG--EANKADNVNLTAKSQ 51
DB 153 KEKALQEAHQQTLDLQAEEDKVNLTAKTK 185

RESULT 13
Q9DGD5 PRELIMINARY; PRT; 1930 AA.
AC Q9DGD5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myosin heavy chain.
OS Pennahia argentata.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sciaenidae; Pennahia.
OX NCBI_TaxID=118565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast muscle;
RA Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.;
RT "cDNA cloning and characterization of the complete primary structure of
RT myosin heavy chain from white croaker fast skeletal muscle.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039672; BAB12571.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRODOM; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
DR NCBI_TaxID=118565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast muscle;
RA Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.;
RT "cDNA cloning and characterization of the complete primary structure of
RT myosin heavy chain from white croaker fast skeletal muscle.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039672; BAB12571.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRODOM; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
DR NCBI_TaxID=118565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast muscle;
RX MEDLINE-97352533; PubMed-9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RL muscle.";
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL: D89991; BAA22068.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
ID Q910C5 PRELIMINARY; PRT; 1931 AA.

Query Match 23.7%; Score 60; DB 13; Length 1930;
Best Local Similarity 42.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

OY 21 KEDNVLVESHEKSLG--EANKADNVNLTAKSQ 51
DB 989 KEKALQEAHQQTLDLQAEEDKVNLTAKTK 1021

RESULT 14
Q910C5 PRELIMINARY; PRT; 1931 AA.
ID Q910C5

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AC Q910C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chick atrial myosin heavy chain.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RA Oana S., Machida S., Furutani Y., Hiratsuka E., Momma K., Takao A.,
RA Matsuoka R.;
RT "Characterization and expression pattern of atrial myosin heavy chain
RT gene in developing chick.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB004801; BAB47399.1; -.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRODOM; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
DR NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast muscle;
RX MEDLINE-97352533; PubMed-9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RL muscle.";
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL: D89991; BAA22068.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
ID Q42352 PRELIMINARY; PRT; 1931 AA.
AC Q42352;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin heavy chain.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast muscle;
RX MEDLINE-97352533; PubMed-9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RL muscle.";
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL: D89991; BAA22068.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.

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SQ SEQUENCE 1931 AA; 221162 MW; 59466B7BD0872DDD CRC64;

Matches	14;	Conservative	8;	Mismatches	9;	Indels	2;	Gaps	1;
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QY 21 KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51

992 KEKKALQEAHQQTLDLQAEEDKVNTLTAKTK 1024

Search completed: October 9, 2003, 08:13:33
Job time : 47.6716 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:57 ; Search time 12.9403 Seconds
(without alignments)
166.755 Million cell updates/sec

Title: US-09-928-048A-5

Perfect score: 253

Sequence: 1 FVALGAPLAPRDAGSORPRK.....KSLGEANKADYVLTAKSQ 51

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	98.0	51	3	US-09-044-536A-7
2	248	98.0	51	4	US-10-002-818-3
3	248	98.0	83	4	US-10-002-818-2
4	248	98.0	84	1	US-07-863-014-2
5	248	98.0	84	1	US-08-332-453-2
6	248	98.0	84	1	US-08-689-190-2
7	248	98.0	84	2	US-08-835-231-9
8	248	98.0	84	2	US-08-805-918-3
9	248	98.0	84	3	US-09-044-536A-36
10	248	98.0	84	3	US-09-108-561-9
11	248	98.0	84	4	US-10-002-818-1
12	248	98.0	84	5	PCT-US95-15800-25
13	243	96.0	84	2	US-08-142-551B-1
14	243	96.0	84	2	US-08-411-726-1
15	238	94.1	84	1	US-07-707-114-1
16	237	93.7	50	2	US-08-142-551B-119
17	209	82.6	78	2	US-08-733-446-1
18	209	82.6	79	2	US-08-733-446-2
19	209	82.6	80	2	US-08-733-446-3
20	209	82.6	81	2	US-08-733-446-4
21	209	82.6	84	2	US-08-733-446-5
22	199	78.7	84	1	US-07-773-098-1
23	199	78.7	84	1	US-07-773-098-2
24	199	78.7	84	1	US-07-773-098-7
25	199	78.7	84	1	US-07-773-098-8
26	199	78.7	84	1	US-07-773-098-9
27	199	78.7	84	1	US-07-773-098-10

28	194	76.7	84	1	US-07-776-272-14
29	59	23.3	419	4	US-09-252-991A-29836
30	58	22.9	1120	4	US-09-147-404-1
31	56	22.1	237	4	US-09-252-991A-19408
32	55	21.7	1886	4	US-08-938-105-3
33	54.5	21.5	740	4	US-09-252-991A-21575
34	54.5	21.5	801	4	US-09-134-001C-5584
35	52.5	20.8	185	3	US-09-154-083-14
36	52	20.6	133	3	US-08-961-083-188
37	52	20.6	133	3	US-09-536-784-188
38	52	20.6	287	1	US-08-624-125-17
39	52	20.6	287	1	US-08-937-155-17
40	51	20.2	135	4	US-09-252-991A-19405
41	51	20.2	212	4	US-09-369-247-88
42	51	20.2	337	4	US-09-252-991A-16886
43	51	20.2	497	4	US-09-252-991A-23620
44	51	20.2	706	1	US-08-339-152A-29
45	51	20.2	706	2	US-08-007-999B-4

ALIGNMENTS

RESULT 1

US-09-044-536A-7
Sequence 7, Application US/09044536A
Patent No. 6025467

GENERAL INFORMATION:

APPLICANT: FUKUDA, Tsunehiko

APPLICANT: NAKAGAWA, Shizue

APPLICANT: HAKASHITA, Junko

APPLICANT: TAKETOMI, Shigehisa

TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 Water Street

CITY: Boston

STATE: Massachusetts

COUNTRY: US

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/044,536A

FILING DATE: 19-MAR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/662,871

FILING DATE: 12-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: CONLIN, David G

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 46509-DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 51 amino acids

TYPE: amino acid

STRANDEDNESS:

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: partial peptide

LOCATION: 1..51

US-09-044-536A-7

Query Match 98.0%; Score 248; DB 3; Length 51;
Best Local Similarity 98.0%; Pred. No. 6.3e-28;

Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 51
|||||
Db 1 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 51

RESULT 2

US-10-002-818-3
; Sequence 3, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hormone
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002,818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-3

Query Match 98.0%; Score 248; DB 4; Length 51;
Best Local Similarity 98.0%; Pred. No. 6.3e-28;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 51
|||||
Db 1 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 51

RESULT 3

US-10-002-818-2
; Sequence 2, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hormone
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002,818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 2
; LENGTH: 83
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-2

Query Match 98.0%; Score 248; DB 4; Length 83;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 51
|||||
Db 33 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 83

RESULT 4

US-07-863-014-2
; Sequence 2, Application US/07863014
; Patent No. 5382658
; GENERAL INFORMATION:
; APPLICANT: KRONIS, K. Anne
; APPLICANT: BOZZATO, Richard P.
; TITLE OF INVENTION: STABILITY-ENHANCED VARIANTS OF
; TITLE OF INVENTION: PARATHYROID HORMONE
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/863,014
; FILING DATE: 19920403
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/163 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-863-014-2

Query Match 98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 51
|||||
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHSKSLGEANKADNVNLTAKSQ 84

RESULT 5

US-08-332-453-2
; Sequence 2, Application US/08332453
; Patent No. 559792
; GENERAL INFORMATION:
; APPLICANT: KRONIS, K. Anne
; APPLICANT: BOZZATO, Richard P.
; TITLE OF INVENTION: BONE-STIMULATING, NON-VASOACTIVE
; TITLE OF INVENTION: PARATHYROID HORMONE VARIANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,453
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,680
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/182 ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-453-2

Query Match 98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 6
US-08-689-190-2
Sequence 2, Application US/08689190
Patent No. 5714349
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, Takao
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41614-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-689-190-2

Query Match 98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 7
US-08-835-231-9
Sequence 9, Application US/08835231
Patent No. 5861284
GENERAL INFORMATION:
APPLICANT: NISHIMURA, Osamu
APPLICANT: KURIYAMA, Masato
APPLICANT: KUYAMA, No. 5861284uyuki
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,231
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41614-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-835-231-9

Query Match 98.0%; Score 248; DB 2; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

LOCATION: 26
OTHER INFORMATION: Xaa- basic amino acid;
FEATURE:
NAME/KEY: Modified-site
LOCATION: 27
OTHER INFORMATION: Xaa- non-charged hydrophilic amino acid,
OTHER INFORMATION: basic amino acid;
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30
OTHER INFORMATION: Xaa- acidic amino acid, aliphatic neutral
OTHER INFORMATION: amino acid;
US-09-044-536A-36

Query Match 98.0%; Score 248; DB 3; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEANKADNVNLTAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEANKADNVNLTAKSQ 84
|||||

RESULT 10

US-09-108-661-9
Sequence 9, Application US/09108661
Patent No. 6287806

GENERAL INFORMATION:

APPLICANT: NISHIMURA, Osamu
APPLICANT: KURIYAMA, Masato
APPLICANT: KOYAMA, No. 6287806uyuki

APPLICANT: FUKUDA, Tsunehiko

TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/108,661

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,709

FILING DATE: 07-DEC-1994

APPLICATION NUMBER: 07/838,857

FILING DATE: 18-FEB-1992

APPLICATION NUMBER: JP 024841

FILING DATE: 19-FEB-1991

APPLICATION NUMBER: JP 0271438

FILING DATE: 18-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: DAVID, RESNICK S

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 41614-FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-09-108-661-9

Query Match 98.0%; Score 248; DB 3; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEANKADNVNLTAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEANKADNVNLTAKSQ 84
|||||

RESULT 11

US-10-002-818-1
Sequence 1, Application US/10002818
Patent No. 6524788

GENERAL INFORMATION:

APPLICANT: Cantor, Thomas L.

TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid
TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/002,818

CURRENT FILING DATE: 2001-11-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Microsoft Word 2000 - ASCII format

SEQ ID NO 1

LENGTH: 84

TYPE: PRT

ORGANISM: human parathyroid hormone peptide fragment

US-10-002-818-1

Query Match

98.0%; Score 248; DB 4; Length 84;

Best Local Similarity 98.0%; Pred. No. 1.2e-27;

Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEANKADNVNLTAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEANKADNVNLTAKSQ 84
|||||

RESULT 12

PCT-US95-15800-25

Sequence 25, Application PC/TUS9515800

GENERAL INFORMATION:

APPLICANT: Blongbraska, Inc.

TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING

TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRUCTS

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 3100 Norwest Center, 90 S. 7th Street

CITY: Minneapolis

STATE: MN

COUNTRY: U.S.A.

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15800

FILING DATE: 07-DEC-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,530

FILING DATE: 07-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.45USWO
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
PCT-US95-15800-25

Query Match 98.0%; Score 248; DB 5; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 84
|||||

RESULT 13

US-08-142-551B-1
Sequence 1, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..84
OTHER INFORMATION: /note= "84 amino acid PTH"
US-08-142-551B-1

Query Match 96.0%; Score 243; DB 2; Length 84;
Best Local Similarity 96.1%; Pred. No. 6.1e-27;
Matches 49; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 84
|||||

RESULT 14

US-08-411-726-1
Sequence 1, Application US/08411726
Patent No. 5880093
GENERAL INFORMATION:
APPLICANT: BAGNOLI, Franco
TITLE OF INVENTION: Use of Parathormone, Its Biologically
TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The Prep
TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment o
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1 Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,726
FILING DATE: 05-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02755
FILING DATE: 08-OCT-1993
APPLICATION NUMBER: MI-92A002331
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: PALMESE, Maria Luisa
REGISTRATION NUMBER: 34,402
REFERENCE/DOCKET NUMBER: 2111/1300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-425-7200
TELEFAX: 212-425-5288
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-411-726-1

Query Match 96.0%; Score 243; DB 2; Length 84;
Best Local Similarity 96.1%; Pred. No. 6.1e-27;
Matches 49; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 84
|||||

RESULT 15
 US-07-707-114-1
 ; Sequence 1, Application US/07707114
 ; Patent No. 5208041
 ; GENERAL INFORMATION:
 ; APPLICANT: SINDREY, Dennis R.
 ; TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID
 ; TITLE OF INVENTION: HORMONE
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/707,114
 ; FILING DATE: 19910523
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 16777/147 ALLE
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 84 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: hPTH
 ; US-07-707-114-1

Query Match 94.1%; Score 238; DB 1; Length 84;
 Best Local Similarity 94.1%; Pred. No. 3, le-26;
 Matches 48; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSQPRKEDNYLVESHEKSLGEANKADYNYLTAKSQ 51
 DB 34 FVALGAPLAPRDAGSQPRKEDNYLVESHEKSLGEADKANYDVLTKAKSQ 84

Search completed: October 9, 2003, 08:15:10
 Job time : 12.9403 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 08:10:52; Search time 95.1493 Seconds
(without alignments)
86.365 Million cell updates/sec

Title: US-09-928-048A-5

Perfect score: 253

Sequence: 1 FVALGAPLAPRDAGSORPRK.....KSLGEANKADYVNLTKAKSQ 51

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	100.0	51	10	US-09-928-047B-3
2	253	100.0	51	12	US-09-928-048A-5
3	253	100.0	57	10	US-09-928-047B-8
4	253	100.0	78	10	US-09-928-047B-4
5	253	100.0	82	10	US-09-928-047B-2
6	253	100.0	83	10	US-09-928-047B-1
7	253	100.0	83	12	US-09-928-048A-4
8	253	100.0	84	12	US-09-928-047B-5
9	253	100.0	84	12	US-09-928-048A-3
10	253	100.0	84	11	US-09-928-047B-1
11	248	98.0	78	11	US-09-928-047B-1
12	248	98.0	84	9	US-09-928-047B-1
13	248	98.0	84	11	US-09-928-047B-1
14	248	98.0	84	11	US-09-928-047B-1
15	248	98.0	115	15	US-10-157-031-50

16	247	97.6	50	10	US-09-928-047B-7	Sequence 7, Appl1
17	247	97.6	50	12	US-09-928-048A-7	Sequence 7, Appl1
18	206	81.4	84	15	US-10-215-770-3	Sequence 3, Appl1
19	199	78.7	84	9	US-09-879-257A-49	Sequence 49, Appl1
20	199	78.7	84	15	US-10-215-770-4	Sequence 4, Appl1
21	194	76.7	84	15	US-10-215-770-2	Sequence 2, Appl1
22	164	64.8	84	11	US-09-843-221A-11	Sequence 11, Appl1
23	160	63.2	84	15	US-10-215-770-5	Sequence 5, Appl1
24	95	37.5	20	12	US-09-928-048A-8	Sequence 8, Appl1
25	68.5	27.1	88	15	US-10-215-770-6	Sequence 6, Appl1
26	61	24.1	557	9	US-09-815-242-12165	Sequence 12165, A
27	61	24.1	563	9	US-09-815-242-5464	Sequence 5464, Ap
28	59	23.3	566	16	US-10-282-287-4	Sequence 4, Appl1
29	59	23.3	537	9	US-09-815-242-12804	Sequence 12804, A
30	57	22.5	238	10	US-09-323-998D-41	Sequence 41, Appl1
31	55.5	21.9	46	9	US-09-864-761-34138	Sequence 34138, A
32	55	21.7	44	11	US-09-843-221A-13	Sequence 13, Appl1
33	55	21.7	1157	10	US-09-935-291A-12	Sequence 12, Appl1
34	55	21.7	1518	10	US-09-801-368-152	Sequence 152, Appl1
35	54	21.3	1033	11	US-09-820-843A-75	Sequence 75, Appl1
36	54	21.3	1075	15	US-10-156-761-10208	Sequence 10208, A
37	52.5	20.8	521	12	US-10-168-651-26	Sequence 26, Appl1
38	52.5	20.8	552	15	US-10-225-567A-430	Sequence 430, App
39	52	20.6	133	9	US-09-765-272-188	Sequence 188, App
40	52	20.6	241	15	US-10-278-173-78	Sequence 78, Appl1
41	52	20.6	287	10	US-09-323-998D-17	Sequence 17, Appl1
42	52	20.6	399	12	US-09-769-744A-94	Sequence 94, Appl1
43	52	20.6	682	9	US-09-815-242-11214	Sequence 11214, A
44	51.5	20.4	425	15	US-10-128-714-3260	Sequence 3260, Ap
45	51.5	20.4	425	15	US-10-128-714-8260	Sequence 8260, Ap

ALIGNMENTS

RESULT 1
US-09-928-047B-3
; Sequence 3, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-3

Query Match 100.0%; Score 253; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.8e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVALGAPLAPRDAGSORPRKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51
DB 1 FVALGAPLAPRDAGSORPRKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51

RESULT 2
US-09-928-048A-5
; Sequence 5, Application US/09928048A
; Publication No. US20030138858A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT

; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20015.00
 ; CURRENT APPLICATION NUMBER: US/09/928,048A
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 51
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-048A-5

Query Match 100.0%; Score 253; DB 12; Length 51;
 Best Local Similarity 100.0%; Pred. No. 7.8e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 51
 Db 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 51

RESULT 3
 US-09-928-047B-8
 ; Sequence 8, Application US/09928047B
 ; Patent No. US20020160945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantor, Thomas
 ; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20002.00
 ; CURRENT APPLICATION NUMBER: US/09/928,047B
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/224,446
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 57
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-047B-8

Query Match 100.0%; Score 253; DB 10; Length 57;
 Best Local Similarity 100.0%; Pred. No. 8.9e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 51
 Db 7 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 57

RESULT 4
 US-09-928-047B-4
 ; Sequence 4, Application US/09928047B
 ; Patent No. US20020160945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantor, Thomas
 ; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20002.00
 ; CURRENT APPLICATION NUMBER: US/09/928,047B
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/224,446
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 78
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-047B-4

Query Match 100.0%; Score 253; DB 10; Length 79;

Best Local Similarity 100.0%; Pred. No. 1.3e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 51
 Db 28 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 78

RESULT 5
 US-09-928-047B-2
 ; Sequence 2, Application US/09928047B
 ; Patent No. US20020160945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantor, Thomas
 ; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20002.00
 ; CURRENT APPLICATION NUMBER: US/09/928,047B
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/224,446
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 82
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-047B-2

Query Match 100.0%; Score 253; DB 10; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 51
 Db 32 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 82

RESULT 6
 US-09-928-047B-1
 ; Sequence 1, Application US/09928047B
 ; Patent No. US20020160945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cantor, Thomas
 ; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20002.00
 ; CURRENT APPLICATION NUMBER: US/09/928,047B
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: US 60/224,446
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 83
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-928-047B-1

Query Match 100.0%; Score 253; DB 10; Length 83;
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 51
 Db 33 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGEANKADVNLTKAKSQ 83

RESULT 7
 US-09-928-048A-4
 ; Sequence 4, Application US/09928048A
 ; Publication No. US20030138858A1
 ; GENERAL INFORMATION:


```

; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-4

Query Match      100.0%; Score 253; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 51
Db 33 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 83

RESULT 8
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-5

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Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 84

RESULT 9
US-09-928-048A-3
; Sequence 3, Application US/09928048A
; Publication No. US20030138658A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-3
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Query Match      100.0%; Score 253; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 84

RESULT 10
US-10-215-770-1
; Sequence 1, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-770-1

Query Match      100.0%; Score 253; DB 15; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLSHESKSLGKANKADVNVLTAKSQ 84

RESULT 11
US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHY
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-12

Query Match      98.0%; Score 248; DB 11; Length 78;
Best Local Similarity 98.0%; Pred. No. 5.8e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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